Acces DR#

- 54659

SEARCH REQUEST FORM

Scientific and Technical Inf rmation Center

Requester's Full Name:			Examiner # :	Date:	
	Number 30				
Mail Box and Bldg/Room Location	on:	Result	s Format Preferred		DISK E-MA
If more than one search is sub	mitted, please	prioritize	searcnes in orde	*********	****
Please provide a detailed statement of the Include the elected species or structures, utility of the invention. Define any term known Please attach a copy of the covered the	keywords, synony is that may have a s	ms, acronyr special mear	ns, and registry numb ling. Give examples o	ers; and combine wi	th the concept or
Title of Invention:		1. S.		A MARKET	
Inventors (please provide full names):					A Company of the Comp
Earliest Priority Filing Date:	Service Service				
For Sequence Searches Only Please incl	lude all pertinent info	ormation (pa	– rent, child, divisional, o	r issued patent numb	ers) along with the
appropriate serial number.					
STAFF USE ONLY	**************************************			**************************************	•
Searcher:	NA Sequence (#)	2	STN		
Searcher Phone #: 4498	AA Sequence (#)	6	Dialog		
Searcher Location:	Structure (#)		Questel/Orbit		
Date Searcher Picked Up: 11 5	Bibliographic _		Dr.Link		
Date Completed:	Litigation		Lexis/Nexis		
Searcher Prep & Review Time:	_ Fulltext		Sequence Systems		
Clerical Prep Time:	Patent Family		WWW/Internet		

Other (specify)_

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSB/gcgdata/genesed/geneseqp/AA1981.DAT:*
3: /SIDSB/gcgdata/genesed/geneseqp/AA1983.DAT:*
4: /SIDSB/gcgdata/genesed/geneseqp/AA1983.DAT:*
5: /SIDSB/gcgdata/genesed/geneseqp/AA1984.DAT:*
6: /SIDSB/gcgdata/genesed/geneseqp/AA1985.DAT:*
7: /SIDSB/gcgdata/genesed/geneseqp/AA1986.DAT:*
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AAY96433 AAY96432	AAY96434 AAY17009	AAY96431	AAY96436	AAY96430	AAY97589	AAY96429	AAB26106	ID	
Rat TGF-beta bindi Murine TGF-beta bi	Bovine TGF-beta bi	Vervet TGF-beta bi	Human TGF-beta bin	Human TGF-beta bin	Human secreted pro		Human DAN/Cerberus	Description	

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serine pro	AAY3		922		7	5
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small	AAW094		206	4.2	9	'n
creted pr	AAW4409		116	4.2	9	4
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Mutant human TGF-b	1 AAY96435		23	10.8	23	2

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RESULT
AAB26106
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                                                                                                              02-MAR-2000; 2000WO-US05537.
                                                                                                                                           21-SEP-2000.
                                                                                                                                                                     WO200055193-A2
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                           gene therapy.
                                                                                                                                                                                                                                         Human; DNA/Cerberus-related protein 6; hDCR6; morphogenic protein;
antagonist; BMP; cell growth; cell differentiation; bone formation;
                                                                                                                                                                                                                                                                                    Human DAN/Cerberus-related protein 6 (hDCR6) (exons 1 and 4).
                                                                                                                                                                                                                                                                                                                                             AAB26106;
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                                                     (REGE-) REGENERON PHARM INC
                                                                                  12-MAR-1999;
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                                                                                  99US-0124118.
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RESULT

AAY96429

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XX OSTE

KW OSTE

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Best Local
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Van Ness J,
                                                                                                                                                                                                                                                                                                                                                                                     osteopathic; trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence comprises the amino acid sequence encoded by exons and 4 of the human DAN/Cerberus-related protein 6 (hDCR6) cooling sequence. The coding sequence was isolated from a human kidnay cDNA library containing exons 1 and 4 of the sequence. HDCR6 is closely related to the DAN and DCR5 proteins, both of which act as antagonists morphogenic proteins such as BMP. It is possible that the hDCR6 gene an protein can be used as immunogens, modulators of cell function, growth and differentiation, to reduce undesirable bone formation, to identify DCR6 binding agents, in diagnosis, and in gene therapy.
                    N-PSDB; AAA29055
                                           WPI; 2000-412321/35
                                                                                                                                                                                                                                                                            08-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA94051
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                                                                                                                                                                                                                                                                                                                                                                                                  transforming growth factor-beta; TGF-beta; binding protein;
herapy; antisense therapy; fracture; bone mineralization.
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This shows the human transforming growth factor-beta (TGF-beta) thinding protein designated hBEER. The cDNA and protein may be used for CC prevention, treatment and diagnosis of diseases associated with CC inappropriate BEER expression. For example, they may be used to treat CC disorders associated with decreased TGF-beta BP expression. The cDNA or CC vectors may be administered to treat diseases by rectifying mutations or CC eletions in a patient's genome that affect the activity of BEER by CC expressing inactive proteins or to supplement the patients own production CC faEER polypeptides. The nucleic acids may be used for recombinant CC production of BEER, gene therapy, antisense therapy as probes for CC diagnostic assays and for functional studies. BEER may be used to raise CC antibodies and for identification of BEER modulators. BEER antagonists CC may be used to increase bone mineral content for the treatment of CC disorders such as osteopenia, osteoporosis, fractures and other CC disorders associated with low mineral content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia, osteoporosis and fractures
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
  213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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Similarity

Length 213;

0

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09-JUN-1999;
20-JUL-1999;
03-AUG-1999;
10-AUG-1999;
17-AUG-1999;
                                                                                                                                                                                             WO200075317-A2
                                                                                                                                                                                                                                                                       Secreted protein; human; PRO protein; neoplastic cell growth; tumour; proliferation; leukaemia; lymphoid malignancy; inflammatory disorder; angiogenic disorder; immunologic disorder; PRO7476.
                                                                                                                                                                                                                                                                                                                                                  Human secreted protein PRO7476.
                                                                                                                    15-MAY-2000;
                                                                                                                                                          14-DEC-2000.
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                                                                                                                    2000WO-US13358
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Query Match Length DB	DB	ID	Description
р :	2199	95.6	2323	89	AF326739	AF326739 Homo sap
2	2128	92.5	2329	9	AX056687	AX056687 Sequence
ω	2061	89.6	2296	89	AF331844	
A	2036	88.5	21501	89	AF326736	
c (5	2036	88.5	94752	85	AC003098	
16	1915	83.2	83.2 151780	72	AC055813	
c 7	661	28.7	177744	75	AC073954	
8	201	8.7	177744	75	AC073954	

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KEYWORDS
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AUTHORS
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Brunkow,M.B., Gardner,J.C., Van Ness,J., Paeper,B.W., Kovacevich,B.R., Proll,S., Skonier,J.E., Zhao,L., Sabo,P.J. Fu,Y.H., Alisch,R.S., Gillett,L., Colbert,T., Tacconi,P., GHamersma,H., Beighton,P. and Mulligan,J.T.
Bone Dysplasia Sclerosteosis Results from Loss of the SOST Product, a Novel Cystine Knot-Containing Protein
Am. J. Hum. Genet. 68 (3), 577-589 (2001)
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LVASCCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRARSAKANQAELENAX"
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/db_xref="taxon:9606"
/chromosome="17"
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Maximum DB
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AAV99912 AAV99911 AAF75343 AAAK60124 AAAK60124 AAAA51398 AAV43042 AAAV43042 AAAV43042 AAAV43066 AAAF97870 AAAF97871 AAZ23895	AAC55918 AAQ925193 AAQ92529 AAC37436 AAA880610 AAT45982 AAV57895 AAV25666 AAZ25666 AAZ25666 AAZ34109 AAC781124	AAA29057 AAA29058 AAA29053 AAA29053 AAA91036 AAA91036 AAA91035 AAA91035 AAA91035 AAA91035 AAA91035 AAA91035 AAA91035 AAA91035 AAA91035 AAA91037 AAA91037 AAA91037 AAA91037 AAA91037 AAA91037 AAA31528 AAA31528 AAA31628
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ALIGNMENTS

AAA29056 RESULT

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AAA29056 standard;

cDNA;

2301 ВP

AAA29056;

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Key
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27-NOV-1998;
                   24-NOV-1999;
                                       08-JUN-2000.
                                                                                                                                      Homo sapiens.
                                                                                                                                                                                               Human TGF-beta binding protein (BEER) variant V10I cDNA
                                                                                                                                                                                                                    12-SEP-2000
                                                           WO200032773-A1
                                                                                                                                                                                                                   (first entry)
98US-0110283
                   99WO-US27990
                                                                           /*tag= a
/label= BEER_variant_V10I
/product= TGF-beta_binding_protein
                                                                                                         Location/Qualifiers 48..689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 118-119; 162pp; English.
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Van Ness J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2301 BP; 569 A; 634 C; 614 G; 484 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This cDNA encodes a variant human transforming growth factor-beta (TGF-beta) binding protein designated BEER V101. The encoded prot
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAX40842	AAC05741	AAA94050	AAA94051	AAA29064	AAA94049	AAA29056	AAA91023	AAA29062	AAA29061	AAA29055	ID	SUMMARIES
Human secreted pro	Human secreted pro	Human DAN/Cerberus	Human DAN/Cerberus	Human TGF-beta bin	Human DAN/Cerberus	Human TGF-beta bin	Human secreted pro	Human TGF-beta bin	Mutant human TGF-b	Human TGF-beta bin	Description	SS

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AAF97871	AAF97870	AAX83006	AAC85482	AAQ73473	AAV43042	AAA51398	AAA60620	AAX60124	AAF75343	AAV99911	AAV99912	AAT51124	AAC78510	AA234109	AAZ25666	AAV57895	AAT45982	AAA80610	AAC37436	AAQ92529	AAQ95193	AAC55918	AAA80642	AAA31528	AAX57405	AAQ33591	AAA94047	AAC99909	AAA94048	AAA91035	AAA94041	AAA94042	AAA91036	AAA29059	AAA29063	AAA29058	AAA29060	AAA29057	
Human neuroblastom	Human neuroblastom	Partial mouse WRN	Murine neuropeptid	Porcine pro-interl	Mus musculus Cgamm	Chromosome 16q tum	Maize Knox1 promot	DNA sequence of th	Human TGF-beta rec			\mathbf{H}	PRO940	Human PRO940 nucle	cocaine	cocaine	Human cocaine and	-		P. communis (pear)	Simple tandem repe	Eucalyptus grandis	Human secreted pro	Plant microsatelli	Rat U3 gene trap d	Microsatellite seq		secreted pr	n hDCR6	for Hu	hDCR6	hDCR6 exon	Probe for Human se	F-beta bir	Murine TGF-beta bi	Murine TGF-beta bi	Bovine TGF-beta bi	Vervet TGF-beta bi	

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This cDNA encodes a human transforming growth factor-beta (TGF-beta) to the chromosome 17q1-21. The cDNA and protein may be used for chromosome 17q1-21. The cDNA and protein may be used for contents associated with treat clisorders associated with descreased TGF-beta BP expression. For example, they may be used to treat clisorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant CC production of BEER, gene therapy, antisense therapy, as probes for CC diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists can be used to increase bone mineral content for the treatment of CC disorders such as osteopenia, osteoporosis, fractures and other CC disorders such as osteopenia, osteoporosis, fractures and other
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Best Local Sim
Matches 2301;
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protein, useful for identifying
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US-09-522-217-55
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US-08-266-451B-1	US-08-841-349-16	US-09-328-111-263	US-08-896-164-18	US-09-245-041-5	US-08-943-731-3	US-08-785-150-1	US-08-972-927-2	US-09-087-465-9	PCT-US96-08295-41	US-08-588-258B-41	US-09-416-150-13	US-08-831-132-13	US-08-332-766A-22	US-08-943-731-121	US-07-952-277A-9	US-08-480-366-9	US-08-074-275-9	US-07-799-828C-9	US-07-922-723A-9	US-09-285-601-3	US-09-213-767-1	US-08-687-080-88
Sequence 1, Appli	Sequence 16, Appl	Sequence 263, App	Sequence 18, Appl	Sequence 5, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 9, Appli	•	Sequence 41, Appl	`	•	Sequence 22, Appl	Sequence 121, App	Sequence 9, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 88, Appl				

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STRANDEDNESS: Since TOPOLOGY: linear MOLECULE TYPE: DNA US-08-332-766A-19
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US-08-332-766A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, DONALD J.
REGISTRATION NUMBER: 25,323
                                                                                                                               TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SIMPLE TANDEM REPEATS NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 861-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 New CITY: Washington
                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                : 597 base pairs
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                                                                                                                                                                      (202)
                 DNA (genomic)
                                                      single
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Patent No. 5646029
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                         TELEFAX: (303)499-8089
TELEX: 49617824
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 893 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Caruthers, Jennie M.
REGISTION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEQUENCES: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Du, He
APPLICANT: Gane, Alison M
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ATTORNEY/AGENT INFORMATION:
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                                                                            NAME/KEY: misc_feature LOCATION: 70..339
OTHER INFORMATION: /note OTHER INFORMATION: seque
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                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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CITY: Boulder
STATE: Colorad
                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 70..138 OTHER INFORMATION: /not OTHER INFORMATION: pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/276,452A FILING DATE: 18-JUL-1994
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                              NAME/KEY:
                                                                                                                                                                                                                                                             LOCATION:
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INFORMATION:
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: United States of America
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5370 Manhattan Circle,
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(303)499-8089
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                                                                            /note= "Amino acids 70-138, 38-53,
and 71-90 are sequences which match the peptide
sequences obtained by protein sequencing"
/note= "Amino acids 40, 50, 74, 76, 80, 81, and
                                                                                                                                                                           peptide"
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Pred. No.
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                                                                                                                                                                                              "Putative secretion signal
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0.014;
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hydroxylated
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; OTHER INFORMATION: US-08-276-452A-66
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US-08-798-744-66/c
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                            NAME: CATULINES 34,464
REGISTRATION NUMBER: 27-9
REFERENCE/DOCKET NUMBER: 27-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8089
TELEFAX: (303)499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             TELEX: 49617824
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sir
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1328 gagagagagagagagagagagaga 1353
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/27/
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Plant Arab
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                                                             FEATURE:
                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patent!
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                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/798,744 FILING DATE: 13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                          NAME/KEY: misc_feature
LOCATION: 70..138
OTHER INFORMATION: /noi
OTHER INFORMATION: pepi
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 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                      LOCATION:
                                                                                                                                                                       NAME/KEY:
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Du, He
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Conservative
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SYSTEM: PC-DOS/MS-DOS
                                misc_feature 70..339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 26; DB 1; 100.0%; Pred. No. 0.014;
/note= "Amino acids 70-138, and 71-90 are sequences which
                                                                           /note= "Putative secretion signal
peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/276,452

 Mismatches

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    which match
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                   38-53,
    the peptide
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Run

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Minimum DB
Maximum DB
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Perfect score:
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seq length:
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000 Compugen
      9b_est8:*
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gb_est7:*
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em_esthum13:*
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em_estin2:*
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9b_est82:*
9b_est84:*
9b_est86:*
9b_est86:*
9b_est86:*
9b_est89:*
9b_est90:*
9b_est100:*
9b_est100:*
9b_est100:*
9b_est106:*
9b_est106:*
9b_est106:*
9b_est106:*
9b_est66:*
9b_est71:*
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9b_est50:
9b_est51:
9b_est52:
9b_est53:
9b_est54:
9b_est55:
9b_est56:
9b_est60:
9b_est60:
9b_est61:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                    gb_est1110: *
gb_htt:111: *
gb_gss_fun: *
em_gss_hum6: *
em_gss_hum6: *
em_gss_hum6: *
em_gss_hum6: *
em_gss_hum7: *
em_gss_hum7: *
em_gss_hum7: *
em_gss_pln:1: *
em_gss_pln:1: *
em_gss_rod3: *
em_gss_rod6: *
gb_gss3: *
gb_
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

; Search time 54.37 Seconds
(without alignments)
298.422 Million cell updates/sec 9, 2001, 15:32:16 November Run on:

US-09-668-021-2 Perfect score: Sequence:

213 1 MQLPLALCLVCLLVHTAFRV......KPRPRARSAKANQAELENAY

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 seqs, 76174552 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database :

PIR_68:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMARKIES	
Result No.	Score	Query	Length	DB	ID	Description
1	80	3.8	428		TVHUEK	transforming prote
7	80	3.8	429	7	JC4965	
3	7	3.3	130	N	D83305	
4	7	3.3	148	~	C83091	
S	7	3,3	183	7	B37410	н
9	7	3.3	197	7	G81057	cal
7	7	3.3	197	7	A81819	
80	7	3.3	305	7	S77397	c
6	7	3.3	312	7	D75344	conserved hypothet
10	7	3.3	321	7	B82892	conserved hypothet
11	7	3.3	328	7	S72647	hypothetical prote
12	7	3.3	398	1	S24802	polyferredoxin 6x2
13	7	3,3	408	7	D70365	fimbrial assembly
14	7	3,3	412	Н	KHHUD	cathepsin D (EC 3.
15	7	3.3	510	7	S62901	legumin 31 precurs
16	7	3.3	512	-1	WMCVFM	inclusion body mat
17	7	3.3	562	~	T05758	hypothetical prote
18	7	3,3	587	7	T16617	
19	7	3.3	602	7	S47880	5
20	7	3.3	632	Н	VGVNSY	surface glycoprote
21	7		681	7	E82812	outer membrane hem
22	7	3.3	781	-	TVFFDF	protein kinase Dra
23	7	3.3	917	7	S15885	hexokinase (EC 2.7
24	7	3.3	946	7	T16297	
25	7	3.3	1940	~	A59287	
26	7		6420	~	T30283	polyketide synthas
27	9	2.8	49	7	S29215	neurotoxin Tx2 - s
28	9		65	7	B25025	malX protein - Kle
29	9	2.8		7	S41672	tightly associated

phosphocarrier pro hypothetical prote osteocalcin precur	apolipopiocein ca unknown protein en hypothetical prote 50s ribosomal prot	hypothetical prote hypothetical prote ribosomal protein	50S ribosomal suburibosomal protein ribosomal protein received and received the rec	yeran, yeran yareu hypothetical prote protein F28K19.8 [50S ribosomal prot	ribosomal protin ribosomal protein 30s ribosomal subu hypothetical prote
E86639 D75271 GECH	13/49/2 G85584 T51524 A82560	T30659 T49144 R5EC22	H85996 C41839 S66512	105320 115239 E96808 D86783	R3EC12 JH0443 E85998 S76185
	102 2 102 2 106 2				124 1 124 2 124 2 124 2
27777	7 7 7 7 7 7 7 7 7 7 7 7 7 9 9 9 9 9 9 9	2, 2, 2, 8, 8, 8,	0 0 0 0 0 0 0 0	, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6,	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
30 31 32	ე ო ო ო ი 4 ო დ	37 38 39	4 4 4 4 0 4 5 4 6	4 4 4 4 4 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6	47 48 50

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RESULT 2
204265
elk1 protein - mouse
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999
C;Accession: JG4965; I48339; I48340; S54908
R;Grevin, D.; Ung, S.; Denhez, F.; Dehem, M.; Quatannens, B.; Begue, A.; Stehelin, D.
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                                                                                                                                                                                                                                                                                                                        Gaps
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5. 3.7;
                                                                                                                                                                                                                                                                                                  3.8%; Score 8; DB 1
100.0%; Pred. No. 3.7
:ive 0; Mismatches
transforming protein elk-1 - human
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                           189 PQKGRKPR 196
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hypothetical protein NMB1656 [imported] - Neisseria meningitidis (strain MC58 serogro C; Species: Neisseria meningitidis C; Species: Neisseria meningitidis (c; Species: Neisseria meningitidis (c; Species: 13. Mar. 2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C; Accession: G81057 R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. Hickey, E.K.; 1809-1815, 2000 A; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 A; A; Mill, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Reference number: A81000; MUID:20175755 A; Reference number: G81057
        C;Date: 15. Sep-2000 #sequence_revision 15. Sep-2000 #text_change 31-Dec-2000 C;Accession: C83091 #sequence_revision 15. Sep-2000 #text_change 31-Dec-2000 C;Accession: C83091 #sequence_revision. M.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, E.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 Mature 406, 959-964, 2000 A;Fille: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: B37410
R; Cam, P.; Jouvin-Marche, E.; LeGuern, C.; Marche, P.N.
Burr. J. Immunol. 20, 1337-1343, 1990
A; Tile: Structure of class II genes in wild mouse Mus saxicola: functional and evolu A; Reference number: A37410; MUID:90316177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-2 class II histocompatibility antigen A-2 beta chain - spiny mouse (Mus saxicola) (
                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004858; GB:AE004091; NID:g9950668; PIDN:AAG07829.1; GSPDB:GN
A;Experimental source: strain PAO1
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A; Molecule type: DNA
A; Residues: 1-183 CCAM>
A; Cross-references: GB: M30158
C; Superfamily: class II histocompatibility antigen; immunoglobulin homology
F; 105-170/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus saxicola
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 20;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%; Score 7; DB 2
100.0%; Pred. No. 17;
Live 0; Mismatches
C; Species: Pseudomonas aeruginosa
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.3
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-148 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-197 <TET>
                                                                                                                                                                                                                                                     A; Accession: C83091
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 ARLLPNA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 EIIPELG 163
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26 ARLLPNA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: PA4441
                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics
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                                                                                                 A; Molecule type: mRNA
A; Residues: 1-429 < GRE>
A; Cross-references: EMBL: X87257; NID:g836634; PIDN:CAA60715.1; PID:g836635
A; Experimental source: embyro
R; Glovane, A.; Pintzas, A.; Maira, S.M.; Sobieszczuk, P.; Wasylyk, B.
Genes Dev. 8, 1502-1513, 1994
A; Title: Net, a new ets transcription factor that is activated by Ras.
A; Reference number: A53837; MUID:95047310
A; Reference number: A53837; MUID:95047310
A; Residues: 1-429 < RES>
A; Residues: 1-429 < RES>
A; Cross-references: EMBL: X87257; NID:g836634; PIDN:CAA60715.1; PID:g836635
A; Accession: 148340
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 5-132, T*, 134-224 < RE2>
A; Cross-references: EMBL: X36939; NID:g535922; PIDN:CAA85391.1; PID:g535923
C; Comment: This protein belongs to the subfamily of ternary complex factor (TCF) which H
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A; Residues: 1-130 <STO>
A; Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AAG06110.1; GSPDB:GN001
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA2722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.; Hickey, M.J.; Br
A.; Larbig, K.; Lim,
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hypothetiùj protein PA441 [imported] - Pseudomonas aeruginosa (strain PAOI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PA2722 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 70/3; 219/3; 363/3; 397/3
C;Superfamily: elk-1 transforming protein; ets DNA-binding domain homology
F;7-86/Domain: ets DNA-binding domain homology <FTS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                       A;Title: Structure and organization of the mouse elkl gene. A;Reference number: JC4965; MUID:97017146
A;Accession: JC4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%; Score 8; DB 2;
100.0%; Pred. No. 3.7;
tive 0; Mismatches
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 PQKGRKPR 196
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SEQUENCE FROM N.A. MEDLINE-89203250; PRao V.N., Huebner K Reddy E.S.P.; P19419; 075606; Q9UJM4; 095058; 01-NOV-1990 (Rel. 16, Created) 01-CCT-2000 (Rel. 40, Last sequence update) 01-CCT-2000 (Rel. 40, Last annotation update) ETS-DOMAIN PROTEIN ELK-1. · · · Arryee D.N.T., Kovar H., "Novel family members HuER71, ELFR, and ELKv among ETS-related genes coexpressed with EMS-FLII in Ewing tumor cell lines.", Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases. Harindranath N., Mills F.C., Mitchell M.P., Meindl A., Max E.B., "The human elk-1 gene family: the functional gene and two process pseudogenes embedded in the IgH locus."; Gene 221:215-224(1998). "elk, Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ELK1 DNA-binding."; Nucleic Acids Res. -!- FUNCTION: STIM MEDLINE=92334979; PubMed=1630903; Janknecht R., Nordheim A.; SEQUENCE FROM N.A. (ISOFORM 2). Aryee D.N.T., Kovar H.; SEQUENCE FROM N.A. MEDLINE=99013876; PubMed=9795224; translocation breakpoints. Science 244:66-70(1989). Submitted SEQUENCE FROM N.A. NCBI_TaxID=9606; Janknecht R., Nordheim A.; "Elk-1 protein domains required for direct and SRF-assisted DOMAINS FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE ALTERNATIVE SUBCELLULAR ELEMENT tissue-specific ets-related genes on chromosomes X and 14 near (JUN-1998) to the EMBL/GenBank/DDBJ Huebner K., Isobe M., Ar-Rushdi A., PRODUCTS: LOCATION: PubMed=2539641; 20:3317-3324(1992). NUCLEAR. 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKV; databases Croce O Euteleostomi; two processed

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STRAIN-C57BL; TISSUE-Embryo;
MEDLINE-97017146; PubMed-8863747;
Grevin D., Ung S., Denhez F., Deh
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Giovane A., Pintzas A., Maira S.-

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Mammalia; Eutheria; Rodentia;
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                                                                                 "Structure and organization Gene 174:185-188(1996).
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Transcription regulation; Activator; Nuclear protein; DNA-binding;
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                                                                                                                                                                        FUNCTION: THIS PROTEIN BINDS SPEC
FUNCTION: THIS PROTEIN BINDS SPEC
IS STIMULATED BY OTHER RIBOSOMAL
IT IS IMPORTANT DURING THE EARLY
                                                                                                               (BY SIMILARITY).
SIMILARITY: BELONGS TO
      European
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TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED I
LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
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                        jht. It is produced through a collaboration
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Maximum DB seq length: 2000000000
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and is
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match Length
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213
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  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_bacteria:*
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Q9PT38
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Oghvad pseudomonas
Ogl243 mus saxicol
Ogsdr7 forsythia x
Oglyb9 neisseria m
Ogl1n0 streptomyce
Ogxf19 arabidopsis
Ogrf19 deinococcus
Ogrf20 urapplasma
Ogl38 methanococc
                                                                                                                                Q9fyq3 oryza sativ
Q9ygd6 oncorhynchu
Q9yt38 oncorhynchu
Q9pt37 oncorhynchu
Q9pt36 oncorhynchu
Q9ft55 arabidopsis
                                                                                                  Q9gtj4 ancylostoma
Q9u9k3 manduca sex
Q9i0c0 pseudomonas
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RESULT Q9FYQ3

Q9FYQ3; PRELIMINARY; Q9FYQ3; O1-MAR-2001 (TYEMBLTel. 16, 01-MAR-2001 (TYEMBLTEL. 16, 01-MAR-2001 (TYEMBLTEL. 16,

Last sequence update)
Last annotation update)

198 AA

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1		mus muscul	092266 simian herp			Q9w060 drosophila	6 schisto	044934 loligo peal	53 aceto	homo	homo	Q9ns56 homo sapien	9 homo	homo	Q20143 caenorhabdi	892 ratt	O43273 homo sapien	Ф	9		gb8 xylel	7 homo	mi2 homo	7	4003	Q21432 caenorhabdi	7	ω	. Q39521 cryptomeria	0	

RESU Q9YG ID AC	Qу Db	Qu Be	QS	R.E.	RT	RA	R ?	R	0 X	8 8	88	SO	DE
RESULT 2 Q9YGD6 ID Q9YGD6 PRELIMINARY; PRT; 276 AA. AC Q9YGD6;	Oy 149 PGGEAPRA 156 Db 83 PGGEAPRA 90	Query Match 3.8%; Score 8; DB 10; L Best Local Similarity 100.0%; Pred. No. 2.7; Matches 8; Conservative 0; Mismatches 0;		RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases			RC STRAIN=CV. NIPPONBARE;			oc magnorrophyta; hrropsida; roares; roaceae; minhartordeae; oryzeae; OC Oryza.			DE HYPOTHETICAL PROTEIN.
		Length 198; ; Indels 0; Gaps 0;	CRC64;	atabases.	nosome 1, PAC					lar (Oldeae; Olyzeae;	nyta; Spermatophyta;		

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RESULT
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Q9PT38;
Q1-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE
OROCITYNCHUS mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhy
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE B.
Oncorhynchus myklss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoste
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
     Oxidoreductase. SEQUENCE 276
                                                                                                                                                                                              EMBL; AF100933; AAD20992.1; HSSP; P50163; 2AE1.
                                                                                                                                                                                                                                                                                                                              Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., I "Cloning and expression of two carbonyl reductase-like hydroxysteroid dehydrogenase cDNAs in ovarian follicles trout (Oncorbynchus mykiss).";
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SEQUENCE 276 AA;
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InterPro; IPR002347; -.
Pfam; PF00106; adh_short; 1.
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Biochem. Biophys. Res. Commun. 255:123-128(1999).
-1- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
                                                     PRINTS; PRO0081; GDHRDH.
PRINTS; PRO0080; SDRFAMILY.
                                                                                                           Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=99185307;
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PRINTS; PR00080; SDRFAMILY.
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                                                                                                                                     InterPro; IPR002198; -. InterPro; IPR002347; -.
                                                                                                                                                                                                                                                                                                               Biochem.
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                                                                                                                                                                                                                                                                              Chem. Biophys. Res. Commun. 255: SIMILARITY: TO THE SHORT-CHAIN
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0; Mismatches
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  134B52054C751C28 CRC64;
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3.7;
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20beta-
s of rainb
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20beta-
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Q9PT37;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                  Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PT36 PRELIMINARY; PRT; 276 AA.

Q9PT36;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE
                                SEQUENCE FROM N.A.

MEDLINB=99185307; PubMed=10082666;

Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;

"Cloning and expression of two carbonyl reductase-like 20beta-
hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow
trout (Oncorhynchus mykiss).";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE B.
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Biochem. Biophys. Res. Commun. 255:123-128(1999).
-!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncor
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PRINTS; PR00080; SDRFAMILY.
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NCBI_TaxID=8022;
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Pred. No.
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-188-930-286
US-09-8582-298-15
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US-08-68-208-16
US-08-588-974-691-4
US-08-588-973-16
US-08-588-976-16
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US-08-60-11-398B-15
US-08-464-051-15
US-08-462-498-15
US-08-60-911-398B-15
US-08-600-911-398B-10
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US-07-960-981-5
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Sequence 56, Appl	Sequence 9, Appli	Sequence 13, Appl	Sequence 13, Appl	278,	Sequence 144, App	Sequence 3, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 22, Appl	Sequence 22, Appl	Sequence 3, Appli	Sequence 23, Appl	Sequence 23, Appl	Sequence 23, Appl	Sequence 23, Appl

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; MOLECULE TYPE: US-08-468-8478-2
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                                                                                                                       TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07068
COMPUTER READABLE FORM:
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
                                                                                                                                                          REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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TELEPHONE: ZU1-JJ
TO TENAX: 201-994-1744
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                                   TOPOLOGY:
                                                STRANDEDNESS:
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                PROTEIN
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Human CCN-Like Growth Factor
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RESULT 3
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                                                                       Sequence 159, Application US/09188930A Patent No. 6150502 GEMERAL INFORMATION:
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Matches
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             APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 201-994-170
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08,
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: LI
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
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SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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COMPOTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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23 AFKNDATEI 31
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REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
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CITY: ROSELAND
STATE: NEW JERSEY
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 Murison, James Greg
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100.0%;
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Human CCN-Like Growth Factor
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                                                                                                                                                                                          Sequence 15, Application US/08582257 Patent No. 5763400
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 286
LENGTH: 206
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 159
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GENERAL INFORMATION:
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Best Local
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APPLICANT: Adams, Michael E.
APPLICANT: Zittan, Dusan
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APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
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TYPE: PRT
                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 9; Conserv
                                       ADDRESSEE: Akin, Gump
STREET: 816 Congress
CITY: Austin
                                                                                                                                                                                                                                                                                                 28 AFKNDATEI 36
COUNTRY: USA
ZIP: 78701
                              STATE:
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6150502
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                                                                                                                                                                                                                                                                                                                                            Conservative
                                                          Gump, Strauss, Hauer & Feld, L.L.P. ress Avenue, Suite 1900
                                                                                                      and Method
29
                                                                                                                  Ecdysis-Triggering Hormone Compositions and Method for Use as Insecticides
                                                                                                                                                                                                                                                                                                                                                        100.0%;
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Length 206; Indels

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APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
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Minimum DB seq length: Maximum DB seq length:
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213
                                                                                                                                                                                                                                                                     Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                    November
                                                                                                                                                                                                                                      219241 seqs,
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Copyright (c) 1993 - 2000 Comp
pir1:*
pir2:*
pir3:*
pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σı	5	4	ω	2	1	No.	j 1
6	o,	6	σ	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	8	8	Score	
2.8		2.8							٠	3 3	3.3	ω. ω	3.3	ა	ω. ω	3.3	ω . ω	3.3	3.3	3.3	3.3	ω .ω	ω .ω	3.3	ω. ω	3.3	з. 8	3.8	Match)
83	72	65	49	6420	1940	946	917	781	681	632	602	587	562	512	510	412	408	398	328	321	312	305	197	197	148	130	429	428	Length	
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S41672	T00523	B25025	S29215	T30283	A59287	T16297	S15885	TVFFDF	E82812	VGVNSY	S47880	T16617	T05758	WMCVFM	S62901	KHHUD	D70365	S24802	S72647	B82892	D75344	S77397	A81819	G81057	C83091	D83305	JC4965	TVHUEK	ID	
	thetical pr	쥬	neurotoxin Tx2 - s	~		al pr			outer membrane hem	surface glycoprote			hypothetical prote	n b	legumin 31 precurs	cathepsin D (EC 3.	fimbrial assembly	polyferredoxin 6x2	hypothetical prote		conserved hypothet	ם		۳		thetical pa		nsforming pro	Description	

50 50	48	47	46	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
9	6	σ	6	6	6	0	6	0	0	Q	6	6	6	σ	δ	σ	6	0	σ
2.8 8																			
$\frac{124}{124}$	124	124	124	121	120	118	118	113	111	110	110	108	106	102	102	100	97	89	88
44	Ν	2	щ.	N	N	2	2	N	Ν	N	ш	N	N	N	Ν	N	Н	N	N
ЈН0807 ЈН0809	E85998	JH0443	R3EC12	D86783	E96808	T15239	T05520	S66512	C41839	н85996	R5EC22	T30659	A82560	T51524	G85584	PC1130	GECH	D75271	E86639
ribosomal protein ribosomal protein	30S ribosomal subu	ribosomal protein	ribosomal protein	50S ribosomal prot	protein F28K19.8 [hypothetical prote	geranylgeranylated	ribosomal protein	ribosomal protein	50S ribosomal subu	ribosomal protein	hypothetical prote	50S ribosomal prot	hypothetical prote	unknown protein en	insulin receptor-r	osteocalcin precur	hypothetical prote	phosphocarrier pro

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JC4965
elk1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999
C;Accession: JC4965; I48339; I48340; S54908
R;Grevin, D.; Ung, S.; Denhez, F.; Dehem, M.; Quatannens, B.; Begue, A.; Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A41354; S54721
R;Rao, V.N.; Huebner, K.; Isobe, M.; ar-Rushdi, A.; Croce, C.M.; Reddy, E.S.P.
Science 244, 66-70, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:119867; OMIM:311040
A;Map position: Xp11.2-Xp11.2
C;Superfamily: elk-1 transforming protein; ets DNA-binding domain homology C;Keywords: DNA binding; oncogene; transforming protein
C;Keywords: DNA binding; oncogene; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
A; Gene: GDB: ELK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: ERK phosphorylation potentiates Elk-1-mediated ternary complex formation and A; Reference number: S54721; MUID:95196758
A; Accession: S54721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M25269; NID:g538208; PIDN:AAA52384.1; PID:g538209 R;Gille, H.; Kortenjann, M.; Thomae, O.; Moomaw, C.; Slaughter, C.; Cobb, EMBO J. 14, 951-962, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: elk, tissue-specific ets-related genes on chromosomes X and 14 near transloc A;Reference number: A41354; MUID:89203250 A;Accession: A41354
                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 318-328,'xx',331;336-364;380-388,'x',390-392,'X',394-400,'xx',403-405,'X'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-428 < RAO>
                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                             310
                                                                                                                                                                                                                                                                                                            189 PQKGRKPR 196
                                                                                                                                                                                                                                                             PQKGRKPR 317
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                      3.8%; 5c.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                          Score 8;
Pred. No.
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S54908
ehem, M.; Quatannens, B.; Begue, A.; Stehelin,
                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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C;Accession: D83305
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
P;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337
A;Accession: D83305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Giovane, A.; Pintzas, A.; Maira, S.M.; Sobieszczuk, Genes Dev. 8, 1502-1513, 1994
A:Title: Net, a new ets transcription factor that is A:Reference number: A53837; MUID:95047310
A:Accession: I48339
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A; Residues: 1-130 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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C;Superfamily: elk-1 transforming protein; ets DNA-binding
F;7-86/Domain: ets DNA-binding domain homology <ETS>
                         C83091
                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AAG06110.1; GSPDB:GN001A;Experimental source: strain PAO1
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hypothetical protein PA4441 [imported] - Pseudomonas aeruginosa
                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PA2722 [imported] - Pseudomonas aeruginosa (strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: embyro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 5-132,'T',134-224 <RE2>
;Cross-references: EMBL:Z36939; NID:g535922; PIDN:CAA85391.1; PID:g535923
;Comment: This protein belongs to the subfamily of ternary complex factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: I48340
A;Status: preliminary; translated from
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Best Local
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Best Local
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                                                                                                                                                       158 KVRLVAS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 PQKGRKPR 196
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Local Similarity 100.0%;
hes 8; Conservative
                                                                                                                12 KVRLVAS 18
                                                                                                                                                                                                                                                                                                              PA2722
                                                                                                                                                                                                  Similarity 7; Conserv
                                                                                                                                                                                                  3.3%;
ilarity 100.0%;
Conservative
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b; Pred. No. 3.8
0; Mismatches
                                                                                                                                                                                                                       Score 7;
Pred. No.
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                                                                                                                                                                                                            DB
16;
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(strain PAO1)
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Larbig,
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K.; Lim,
                                                                                C;Accession: A81819
R;Parkhill, J.; Achtman, M.;
Holroyd, S.; Jagels, K.; L.
Nature 404, 502-506, 2000
                                                                                                                                                                       hypothetical protein NMA1913 [imported] - Neisseria meningitidis (strain 22491 C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
G81057
                    A; Reference number: A81775; A; Accession: A81819
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A; Gene: NME
                                                             A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
                                                                                                                                                                                                                                              A81819
                                                                                                                                                                                                                                                                   RESULT
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A; Molecule type: DNA
A; Residues: 1-197 <TET>
                                                                                                                                                                                                                                                                                                                         R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eiser Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein NMB1656 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: G81057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83091
                                                                                                                                                             A; Experimental source:
                                                                                                                                                                              A; Cross-references: GB: AE002516;
                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                  A; Accession: G81057
                                                                                                                                                                                                                                                                       A; Reference number: A81000;
                                                                                                                                                                                                                                                                                        A; Title: Complete genome
                                                                                                                                                                                                                                                                                                           A; Authors: Grandi, G.; Sun, L.; Smith, H.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Complete genome see A; Reference number: A82950; A; Accession: C83091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE004858; GB:AE004091; NID:g9950668; PIDN:AAG07829.1; GSPDB:GN
                                                   Query Match
Best Local
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Best Local
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203 KANQAEL 209
                                                 Local Similarity
                                                                                                                             NMB1656
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                                    Conservative
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                            3.38; su
100.08; Pi
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30; MUID:20437337
                                                                                                                                                                                                                                                                                          sequence
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                                                                                                                                                                                                                                                                           MUID:20175755
                                  s; Score 7; DB 2
s; Pred. No. 22;
0; Mismatches
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                                                                                                                                                                                                                                                                                          of Neisseria
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                                         DB .
22;
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17;
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                                  0;
                                                                    Length 197;
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                                                                                                                                                                                                                                                                                                          Moxon,
                                                                                                                                                                                                                                                                                          foxon, E.R.;
serogroup B
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A.; Larbig,
                                  Gaps
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.; Leather,

K.D.; Bentley, S.; Moule, S.;

S.D.; Churcher, C.;
Mungall, K.; Quail,

Klee, M.A.;

S.R.; Mo Rajandre

serogr

MUID: 20222556

Run 8

on:

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Minimum
Maximum
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Perfect score:
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Match
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213
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     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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235.141 Million cell updates/sec
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4 human immun
7 escherichia
8 phytoplasma
9 meriones un
9 gallus gall
6 saccharomyc
4 saccharomyc
9 gallus gall
10 homo sapien
7 kluyveromyc
1 methanobact
1 haemophilus
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2 klebsiella
2 klebsiella
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3 gascherichia
3 escholeplasma
6 spiroplasma
6 thermus aqu
1 homo sapien
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067060 aquifex aeo	Q9z9j0 bacillus ha	P57293 buchnera ap	P48004 rattus norv	013268 gallus gall	P48534 pisum sativ	Q9z2u0 mus musculu	014818 homo sapien	Q9pvy6 xenopus lae	Q9pvq1 xenopus lae	Q29491 macroscelid	P53223 saccharomyc	P54846 mus musculu	P98173 homo sapien	P75290 mycoplasma	070627 mus musculu	060258 homo sapien	

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SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE C FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE C ELEMENT.	~ ~ ~
-!- FUNCTION: STIM	~ C
DNA-binding.";	3 (3)
VA Janknecht R., Nordheim A.; VA "Flk-1 protein domains required for direct and SRF-assisted	3 6
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ	~ :
Novel family members HuER71, ELFR, and ELKv among ETS-related genes T coexpressed with EWS-FIII in Ewing tumor cell lines.":	: : : ' \
Aryee D.N.T., Kovar H.;	~ (
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Harindranath N., Mills F.C., Mitchell M.P., Meindl A., Mai	: ~
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SD GEOTIENCE EXOM N A	≃ ≏
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translocation breakpoints.";	~
Y "elk, tissue-specific ets-related genes on chromosomes X and 14 near	: 3 6
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MEDLINE=89203250; Pubm	~
(N [1] RP SEQUENCE FROM N.A.	~ ^
NCBI_TaxID=9606;	- ~
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;	\simeq
)C = Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Futeleostomi:	× >
	- 22
ETS-DOMAIN PROTEIN ELK-1.	\simeq
)T 01-0CT-2000 (Rel. 40, Last sequence update)	٧,
01-NOV-1990 (Rel. 16, Creat	: :<
P19419; 075606; Q9UJM4; 095058;	7 5
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RESULT 2
ELK1_MOUSE
ID ELK1_M
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Best Local S
Matches 8
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P41969;
01-NOV-1995 (Rel. 32, C
01-OCT-1996 (Rel. 34, I
15-JUL-1999 (Rel. 38, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M25269; AAA52384.1; -. EMBL; AF080616; AAC82466.1; -. EMBL; AL009172; CAA15659.1; -. EMBL; AF000672; AAD00862.1; -. PIR; A41354; TVHUEK.
HSSP; P14921; 2STW.
                                                                       STRAIN-C57BL; TISSUE-Embryo;

MEDLINE-97017146; PubMed-8863747;

Grevin D., Ung S., Denhez F., Deh

Stehelin D., Martin P.;

"Structure and organization of th
                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Activator; Nuclear protein; DN
Phosphorylation; Alternative splicing.
DNA_BIND_ 5 86 ETS_DOMAIN.
DNA_BIND_ 5 86 ETS_DOMAIN.
VARSPLIC 91 95 VAGCS -> SHCAP (IN ISOFORM VARSPLIC 96 428 MISSING (IN ISOFORM 2).
CONFLICT 183 183 S -> N (IN REF. 1).
SEQUENCE 428 AA; 44888 MW; 68F71F8ADB9D3BCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000418; --
pfam; PF00178; Ets; 1
prints; pr00454; ETSDOMAIN.
pr0SITE; PS00345; ETS_DOMAIN_1; 1.
pr0SITE; PS00346; ETS_DOMAIN_2; 1.
pr0SITE; PS00346; ETS_DOMAIN_3; 1.
pr0SITE; PS0061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
Giovane A., Pintzas A., Maira S.-M., "Net, a new ets transcription factor
                                                                                                             (1)
SEQUENCE FROM N.A.
STRAIN-C57BL; TISSUE-Embryo;
                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                    Mus musculus (Mouse).
                     TISSUE-Embryo;
MEDLINE-95047310;
                                                                                                                                                    NCBI_TaxID-10090;
                                                                                                                                                                                                          ETS-DOMAIN PROTEIN ELK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 311040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T00250; -.
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                                                                 Gene
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                                            SEQUENCE OF 5-224
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                                                                                                                                                                                                                                                                                                                                       189 PQKGRKPR 196
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TISSUE SPECIFICITY: LUNG AND TESTIS.
PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND ERK
                                                                174:185-188(1996).
                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                               STANDARD;
                      PubMed=7958835;
                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     3.8%;
                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                      Score 8; Pred. No
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                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                           mouse
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Sobieszczuk P., Wasylyk B.; that is activated by Ras.";
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                                                                                               Quatannens B.,
                                                                          elk1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                Length 428
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30-MAY-2000 (Rel. 30-MAY-2000) (Rel. 30-MAY-2000 (Rel. 30-MAY-2000) (Rel. 30-MAY-2000) (Rel. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  operon.
FEMS Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20088835; PubMed=10620683; Zuerner R.L., Hartskeerl R.A., van de Kemp H., Bal A.E.; "Characterization of the Leptospira interrogans S10-spc-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation.
DNA_BIND 5
CONFLICT 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000418; -. Pfam; PF00178; Ets; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X87257; CAA60715.1;
EMBL; Z36939; CAA85391.1;
HSSP; P14921; 2STW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
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-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes Dev. 8:1502-1513(1994).

-i- FUNCTION: SYIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Spirochaetales;
NCBI_TaxID=173;
                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SEROVAR LAI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:101833; Elk1.
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                                                                                                                                                                                                                                                                                                                             FUNCTION: THIS PROTEIN BINDS SPECIFICALLY TO 23S RRNA; ITS BINDING IS STIMULATED BY OTHER RIBOSOMAL PROTEINS, E.G., L4, L17, AND L20. IT IS IMPORTANT DURING THE EARLY STAGES OF 50S RECONSTITUTION
ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                              (BY SIMILARITY)
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L PROTEIN L22.
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ETS_DOMAIN_2; 1.
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L22.
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B61B5B977731D54F CRC64;
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sp_unclassified:*
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sp_virus:*
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Ogitj4 ancylostoma
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Q9ygd6 oncorhynchu
Q9pt38 oncorhynchu
Q9pt37 oncorhynchu
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Q75770 homo sapien
Q9nq38 homo sapien
Q9nq38 homo sapien
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ALIGNMENTS

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RESULT
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Q9FYQ3;
01-MAR-2001 (TIEMBLIEL 16, C
01-MAR-2001 (TIEMBLIEL 16, L
01-MAR-2001 (TIEMBLIEL 16, L
HYPOTHETICAL PROTEIN.
Q9YGD6
Q9YGD6;
                                                                                                                                                                           Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP002539; BAB08182.1; ... SEQUENCE 198 AA; 21843 MW; 11D1D90FE4B72F4E CRC64;
                                                                                                                                                                                                              STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto DNA, chromosome 1,
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0433F09.";
                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                   149 PGGEAPRA 156
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Q9PT38;
01-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last annotation update)
01-MAY-2001 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 16, Last sequence update)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebarata; Euteleostomi;
Acthopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE B.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-99183307; PubMed-10082666;

Guan G.J., Tanaka M., Todo T., Young G.,

"Cloning and expression of two carbonyl I

hydroxysteroid dehydrogenase cDNAs in ova
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PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
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trout (Oncorhynchus mykiss).";
Biochem. Biophys. Res. Commun. 255:123-128(1999).
-!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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                                                                                                                                                                                                                                                                      Biochem.
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HSSP; P50163; 2
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                       PRINTS; PRO0080; SDRFAMILY.
                                                                  PRINTS;
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                                                                                                                    InterPro; IPR002198; -. InterPro; IPR002347; -.
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                                                                                                                                                                                                                                            ut (Oncorhynchus mykiss).";
chem. Biophys. Res. Commun. 255:123-128(1999).
SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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30239 MW;
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0; Mismatches
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134B52054C751C28 CRC64;
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20beta-
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01-MAY-2000
01-MAR-2001
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Q9PT37;
SEQUENCE FROM N.A.

MEDLINE=99185307; PubMed=10082666;
Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;

"Cloning and expression of two carbonyl reductase-like 20beta-
"Cloning and expression of two carbonyl reductase-like 20beta-
hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss).";

Biochem. Biophys. Res. Commun. 255:123-128(1999).
                                                                                                                                                                                                              Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii, Neopterygii; Teleostai; Euteleostai;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncor
                                                                                                                                                                                                                                                                                                                                   O9PT36
O9PT36; PRELIMINARY;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16.
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InterPro;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE
                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase. SEGUENCE 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trout (Oncorhynchus mykiss).";
Biochem. Biophys. Res. Commun. 255:123-128(1999)
-!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., I
"Cloning and expression of two carbonyl reductase-like inductive the carbonyl reductase in the control of the carbonyl reductase."
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PRINTS; PRO0080; SDRFAMILY.
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IPR002347; -.
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Maximum DB
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2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
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Copyright (c) 1993 - 2000 Comp
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AAY96436
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                                                                                                 Human TGF-beta bin
Human TGF-beta bin
Human DAN/Cerberus
Human TGF-beta bin
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Human neuroendocri	AAY21476	19	19	2.8	0	
Peptide recognised	AAW45613	£1	T.	•	6	
	18	19	15	2.8	. 0	
entricu	1	12	10	- 1	6	
AS-30D tumour Type	~	18	917	ω .ω	7	
Rat hexokinase II.	AAW37429	18	917	ω . ω	7	
Rat hexokinase II.	43	18	917		7	
HSV-2 strain SB5 C	AAW72072	19	718	•	7	
ta	AAB53197	21	457	ω ω	7	
Human secreted pro	AAB64892	22	426	ω ω	7	
Amino acid sequenc	AAY93685	21	412		7	
Human tumour-assoc	AAY06478	20	412	٠	7	
Death associated p	AAW71369	19	412	ω . ω	7	
. Human death associ	AAR74207	16	412	ω . ω	7	
Cat flea HMT perit	AAB29625	21	285	ω. ω	7	
_	AAG42283	21	282	3.3	7	
Arabidopsis thalia	AAG42284	21	265	ω. 3	7	
	AAG42285	21	219		7	
Forsythia dirigent	AAW65018	19	186	3.3	7	
rο	AAB43980	21	173		7	
Human secreted pro	AAG00348	21	61	٠	7	
Serine protease in	AAB46589	22	1064		8	
Serine protease in	AAB46588	22	1064		8	
Human serine prote	AAY33002	20	922		8	
Human secreted pro	AAY36226	20	554		8	
٠	AAY32824	20	428		8	
-i p	AAY52704	20	428		8	
Human serine prote	AAY33001	20	177		8	
	AAB55970	22	206	4.2	9	
cell protein	AAB55920	22	206	4.2	9	
Murine skin cell p	AAY76031	21	206	4.2	9	
Murine skin cell p	AAY75981	21	206	4.2	9	
Human adult retina	AAB10233	21	206	4.2	9	
Homo sapiens fetal	AAW95711	20	206	4.2	9	
Human small CCN-li	AAW58704	19	206	4.2	9	
Human small CCN-li	AAW09408	18	206	4.2	9	
O	AAW44090	18	116	4.2	9	
Secreted protein A	76	18	116	4.2	9	
Mutant human TGF-b	AAY96435	21	23	6.1	13	

ALIGNMENTS

RESULT AAY96430

AAY96430 standard; Protein;

213

AΑ

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Location/Qualifiers
                                                                                                                                                osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; variant; V101; gene therapy; antisense therapy; fracture; chromosome 17q12-21; bone mineralization.
27-NOV-1998;
                  24-NOV-1999;
                                     08-JUN-2000.
                                                                                                                               Homo
                                                                                                                                                                                    Human TGF-beta binding protein (BEER) variant V10I.
                                                                                                                                                                                                        12-SEP-2000
                                                                                                                                                                                                                            AAY96430;
                                                      WO200032773-A1
                                                                                                                              sapiens.
                                                                                                                                                                                                        (first entry)
98US-0110283
                  99WO-US27990
                                                                        /note= "wild type valine has been substituted with
    isoleucine"
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AAB26105 AAY96431

AAY96434 AAY9643

Human secreted pro Human DAN/Cerberus Vervet TGF-beta bi Bovine TGF-beta bindi Rat TGF-beta bindi Murine TGF-beta bi

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RESULT
AAY96436
ID AAY9
XX AAY9
AC AAY9
XX AAY9
XX BEER
KW OSTE
KW Chro
XX Chr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone interal content for the treatment of discreters.
                                                                                                                                                                                                              Human TGF-beta binding protein (BEER) variant P38R.
                                                        Homo
                                                                                                           chromosome 17q12-21;
                                                                                                                                     osteopathic; to
BEER; variant;
                                                                                                                                                                                                                                                                          12-SEP-2000
                                                                                                                                                                                                                                                                                                                                   AAY96436;
                                                                                                                                                                                                                                                                                                                                                                                      AAY96436 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis and fractures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brunkow ME,
Van Ness J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoleucine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dfgteaarpqkgrkprprarsakanqaelenay 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFGTEAARPQKGRKPRPRARSAKANQAELENAY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rgkwwrpsgpdfrcipdryragrvqllcpggeaprarkvrlvasckckrltrfhngselk 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGKWWRPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRFHNQSELK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-412321/35.
DB; AAA29056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a variant human transforming growth factor-beta (TGF-beta) otein designated BEER V10I, which comprises a substitution of for the wild-type valine at residue 10. The cDNA and protein for prevention, treatment and diagnosis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galas Do
Winkler
                                                                                                                                                              transforming
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                        P38R;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                딛
                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                        gene
bone
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                                                                                                        growth factor-beta; TGF-bet, therapy; antisense therapy; mineralization.
                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 213; DB 21;
Pred. No. 4.5e-214;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                           TGF-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paeper BW;
                                                                                                                                  a; binding
fracture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                         protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT
AAB26106
ID AAB2
XX

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AAB26106 standard;

Protein;

213 ΑĀ

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Ωy
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                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 203; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         comprises a substitution of arginine for the wild-type proline at residue 38. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGP-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antisodies and for
                                                                                                                                                                                                                                                                                                                                                                              identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such exterior osteopenia, osteoporosis, fractures and other disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia,
                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                  low mineral content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This shows a variant human transforming growth factor-beta (TGF-beta) binding protein designated BEER P38R. The encoderated beta protein designated beta page 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brunkow ME,
Van Ness J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DARW-) DARWIN DISCOVERY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200032773-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                191
                                                                131
                                                                              131 DFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQ
   191
                                                                                                                                                                                    KGRKPRPRARSAKANQAELENAY 213
                                                                                                                                           ETKDVSEYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRGKWWRPSGP 130
                                                                                                                         etkdvseyscrelhftryvtdgpcrsakpvtelvcsgqcgparllpnaigrgkwwrpsgp
kgrkprprarsakangaelenay 213
                                                           \tt dfrcipdryraqrvqllcpggeaprarkvrlvasckckrltrfhnqselkdfgteaarpq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-412321/35
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                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and fractures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galas DJ,
Winkler DG;
                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0110283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38
/label= p38R
/note= "wild type proline has been substituted with arginine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US27990
                                                                                                                                                                                                                                                                     95.3%; Score 203; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kovacevich B,
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                      1.2e-203;
                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                                    Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The encoded protein
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                                                                                                                                                                                                                                                      0;
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                                                                                             190
                                                              190
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0;

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vord size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                        Score
     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                       Match
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Gapop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               November 9, 2001, 15:35:22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MQLPLALCLICLLVHTAFRV.....KPRPRARSAKANQAELENAY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0 ,
    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapext 60.0
                                    US-08-468-847B-2
US-08-468-847B-20
US-09-188-930-286
US-09-188-930-286
US-09-188-930-286
US-09-2475-316A-13
US-08-268-007A-12
US-08-974-691-4
US-08-98-974-691-4
US-08-98-974-691-5
US-08-974-691-5
US-08-974-691-5
US-08-974-691-5
US-08-974-691-5
US-08-974-691-5
US-08-974-691-5
US-08-97-91-5
US-08-97-91-3
US-08-462-498-15
US-08-462-498-15
US-08-554-385-14
US-08-600-911-30
US-08-600-981-5
US-08-960-991-3
US-08-960-991-3
US-08-960-991-3
                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.5
Compugen Ltd.
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Sequence 2, Appli Sequence 15, Appli Sequence 15, Appli Sequence 17, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 13, Appli Sequence 13, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 30, Appli Sequence 32, Appli
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                         ; MOLECULE TYPE: US-08-468-847B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-468-847B-2
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Sequence 2, Application US/08468847B Patent No. 5780263
                                                                                                                                                   APPLICATION NUMBER: US/08/468
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-94-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                   TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 2:
                                                          SEQUENCE CHARACTERISTICS
LENGTH: 206 AMINO ACII
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hastings, TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NEW COUNTRY: US ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, BDDRESSEE: CECCHL, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND
                                    STRANDEDNESS:
                                                      AMINO ACIDS
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Human CCN-Like Growth Factor
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Length 206;

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STRANDEDNESS:
; TOPOLOGY: LIN
; MOLECULE TYPE:
US-08-468-8478-20
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US-08-468-847B-20
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Matches 9
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Best Local S
Matches 9
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOSTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: HU
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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STATE: NEW JERSEY
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les 9; Conserv
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TYPE: AMINO ACID
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; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTMARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 159
; SEQ ID NO 159
; LENGTH: 206
; TYPE: PAT
; ORGANISM: mouse
US-09-188-930-159
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US-09-188-930-286
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Best Local Similarity
"heres 9; Conserv
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LENGTH: 206
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                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
TITLE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SOFTWARE: FastSEQ for Windows Version 3.0
CURRENT APPLICATION NUMBER: US/09/475,316A CURRENT FILING DATE: 1999-12-30
                              TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICIRESINOL REDUCTASES, TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE FILE REFERENCE: WSUR-1-13793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                    Gang, David R.
Sarkanen, Simo
Ford, Joshua D
                                                                                                                                         Dinkova-Kostova, Albena T.
Fujita, Masayuki
                                                                                                                                                                            Lewis, No. 6210942man G. Davin, Laurence B.
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100.0%; Pred. No. 0.29;
Live 0; Mismatches
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Maximum DB seq length: 200000000
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Perfect score:
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   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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T05520	866512	C41839	н85996	R5EC22	T49144	A82560	T51524	G85584	I57492	D75271	S41672	B25025	S29215	JP0066	T30283	A59287	T15280	MWAXIC	C81060	A81817
geranylgeranylated	ribosomal protein	ribosomal protein	50s ribosomal subu	ribosomal protein	hypothetical prote	50s ribosomal prot	hypothetical prote	unknown protein en	apolipoprotein C-I	hypothetical prote	tightly associated	malX protein - Kle	neurotoxin Tx2 - s	ribosomal protein	polyketide synthas	myosin heavy chain	hypothetical prote	myosin heavy chain	translation initia	translation initia

JC4965 ELKI protein - mouse C:Species: Mus musculus (house mouse) C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999 C:Accession: JC4965; I48339; I48340; S54908 R:Grevin, D.; Ung, S.; Denhez, F.; Dehem, M.; Quatannens, B.; Begue, A.; Stehelin, A;Cross-references: GDB:119867; OMIN:311040 A;Map position: Xp11.2-Xp11.2 C;Superfamily: elk-1 transforming protein; ets DNA-binding domain homology C;Keywords: DNA binding; oncogene; transforming protein F;7-86/Domain: ets DNA-binding domain homology <FTS> A; Molecule type: mRNA A; Residues: 1-428 (RAO) A; Cross-references: GB: M25269; NID: g538208; PIDN: AAA52384.1; PID: g538209 A; Cross-references: GB: M25269; NID: g538208; PIDN: AAA52384.1; PID: g538209 R; Gille, H.; Kortenjann, M.; Thomae, O.; Moomaw, C.; Slaughter, C.; Cobb, M.H.; Shaw, EMBO J. 14, 951-962, 1995 A; Title: ERK phosphorylation potentiates Elk-1-mediated ternary complex formation and A; Reference number: S54721; MUID: 95196758 A; Accession: S54721 C;Species: Homo sapiens (man) C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999 C;Accession: A41354; S54721 밁 A; Molecule type: protein A; Residues: 318-328,'XX',331;336-364;380-388,'X',390-392,'X',394-400,'XX',403-405,'X' C; Genetics: A;Title: elk, tissue-specific ets-related A;Reference number: A41354; MUID:89203250 A;Accession: A41354 R;Rao, V.N.; Huebner, K.; Isobe, M.; ar-Rushdi, A.; Croce, C.M.; Reddy, E.S.P. Science 244, 66-70, 1989 RESULT Ş A; Gene: GDB: ELK1 A; Status: preliminary transforming Query Match Best Local Matches 310 189 PQKGRKPR 196 Local Similarity hes 8; Conser N PQKGRKPR 317 protein elk-1 - human Conservative 3.8%; 0; Score 8; Pred. No. Mismatches genes on chromosomes X and 14 near transloc DB 1; Length 428; Indels 0 Gaps 0;

D.

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A:Cross-references: DDBJ:AB005060; NID:g2626738; PIDN:BAA23417.1; PID:g2626739 A:Experimental source: SK-NSH cell C:Comment: This protein is a member of the epidermal growth factor family. It ating the differentiation of MDA-MB-453 cells.
C:Superfamily: unassigned EGF-related proteins; EGF homology C:Keywords: glycoprotein
                                                                                                                                                                                                             F;258-311/Domain: Ig-like #status predicted <IGL>
F;345-381/Domain: EGF homology <EGF9
F;345-381/Domain: EGF-like #status predicted <EGF2>
F;346-381/Domain: EGF-like #status predicted <EGF2>
F;147,278,451/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ErbB kinase activator alpha, brain and thymus - human C; Species: Homo sapiens (man) C; Date: 25.Nov-1997 #sequence_revision 25-Nov-1997 #text_change 21-Jul-2000
                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Blochem. 122, 675-680, 1997
A;Title: A novel brain-derived member of the epidermal growth factor family that interach; Reference number: JC5700; MUID:98006324
A;Accession: JC5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 70/3; 219/3; 363/3; 397/3
C;Superfamily: elk-1 transforming protein; ets DNA-binding
F;7-86/Domain: ets DNA-binding domain homology <ETS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: embyro R;Giovane, A.; Pintzas, A.; Maira, S.M.; Sobieszczuk, P.; Wasylyk, B. Genes Dev. 8, 1502-1513, 1994
A;Title: Net, a new ets transcription factor that is activated by Ras A;Reference number: A53837; MUID:95047310
A;Accession: 148339
       В
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A; Residues: 1-850 <HIG>
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A;Title: Structure and organization of the mouse elkl gene
A;Reference number: JC4965; MUID:97017146
A;Accession: JC4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown
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A; Residues: 1-429 < RES>
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A; Residues: 1-429 <GRE>
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Local Similarity 100.0%;
les 8; Conservative (
       PRPRARGA 732
                                                  PRPRARGA 202
                                                                                                 Similarity
8; Conser
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s; Pred. No. 3.8
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                                             C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_c
C;Accession: D83305
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Polger, F.
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                      RESULT
D83305
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A; Residues: 1-119 <KUL>
C; Superfamily: GAL4 zinc
F; 7-54/Domain: GAL4 zinc
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A; Reference number: A82950; MUID: 20437337
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GAL4 zinc
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15-Sep-2000 #text_change 31-Dec-2000

(strain PAO1)

K.R.;

Kas,

A.;

Larbig,

X.;

Warrener, P.; Hickey,

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transcription activator - Emericella nidulans ()Species: Emericella nidulans, Aspergillus nidulans c:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #tex C:Accession: S14292 R.Kulmburg, P.; Prange, T.; Mathieu, M.; Sequeval, D.; FEBS Lett. 280, 11-16, 1991 A;Title: Correct intron splicing generates a new type o A;Reference number: S14292; MUID:91184391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: necessary for the expression of MHC class I histoc;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterodimer F;18-82/Domain: immunoglobulin homology <IMM>F;25-80/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-2-microglobulin - guinea pig
N;Alternate names: class I histocompatibility antigen beta chain
C;Species: Cavia porcellus (guinea pig)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Jan-1997
C;Accession: A02181
C;R;Wolfe, P.B.; Cebra, J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Immunol. 17, 1493-1505, 1980
A; Title: The primary structure of guinea pig beta2-microglobulin
A; Reference number: A02181; MUID:82057805
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TX2.5_PHONI
LHA1_RHOAC
MALX_KLEPN
VE7_HPV44
APC2_MACFA
APC2_MACFA
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219_HUMAN
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AT TOMEWER	FGFH_MOUSE	FGFH_HUMAN	PYRE_HAEIN	TRPF_KLULA	RETB_CHICK	HS72_CANAL	YCYO_YEAST	RL6A_YEAST	TRIC_CHICK	B3AR_MERUN	R19E_PYRHO	RK22_ORYSA	RK22_MAIZE	YIIR_ECOLI	IL4_SHEEP	IL4_CAPHI	IL4_BOVIN
	070627 mus musculu	060258 homo sapien	P43855 haemophilus	P13997 kluyveromyc	P41263 gallus gall	P46587 candida alb		Q02326 saccharomyc	P27673 gallus gall	070432 meriones un	059041 pyrococcus	P12140 oryza sativ	P06589 zea mays (m.	P32161 escherichia	P30368 ovis aries	P79155 capra hircu	P30367 bos taurus

RA Rao V.N., Hubbner K., Isobe M., Ar-Rushdi A., Croce C.M., RA Reddy E.S.P.; RT "elk, tissue-specific ets-related genes on chromosomes X and 14 near RT translocation breakpoints."; RL Science 244:66-70(1989). RN SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RN Harindranath N., Mills F.C., Mitchell M.P., Meindl A., Max E.E.; RT "The human elk-1 gene family: the functional gene and two processed RT gene 221:215-224(1998). RT Gene 221:215-224(1998). RN [3] RP SEQUENCE FROM N.A. RA Grafham D.; RN SEQUENCE FROM N.A. (ISOFORM 2). RA Grafham D.; RN SEQUENCE FROM N.A. (ISOFORM 2). RA Arvee D.N.T., KOVAI H.; RA Arvee D.N.T., KOVAI H.; RT "Novel family members HuER71, ELFR, and ELKV among ETS-related genes RT Coexpressed with EWS-FIII in Exing tumor cell lines."; RN SEQUENCE STRANSCRIPTION GENERAL SUBMITTER SERUM RESPONSE RN Jahknecht R., Nordheim A.; RN Jahknecht R., Nordheim A.; RN "Elk-1 protein domains required for direct and SRF-assisted DNA-Dinding."; Nucleic Acids Res. 20:3317-3324(1992). RELEMENT. CC -I- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKV; ARE	SULT 1 KI_HUMAN ELK1_HUMAN P19419; O75606; Q9UJM4; O95058; O1-NOV-1990 (Rel. 16, Created) O1-CCT-2000 (Rel. 40, Last sequence update) O1-CCT-2000 (Rel. 40, Last annotation update) ETS-DOMAIN PROTEIN ELK-1. ELK1. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=89203250; PubMed=2539641; SEQUENCE FROM N.A.
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Best Local S
Matches
                                                                                                                                                                                                                                                                      ELK1_MOUSE
P41969;
01-NOV-1995
01-OCT-1996
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PRO7 entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000418; -.

Pfam; PF00178; Ets; 1.

PRINTS; PR00454; ETS_DOMAIN_1; 1.

PROSITE; PS00345; ETS_DOMAIN_2; 1.

PROSITE; PS00346; ETS_DOMAIN_2; 1.

PROSITE; PS50061; ETS_DOMAIN_3; 1.

Transcription regulation; Activator; Nuclear protein; DNA-binding; Phosphorylation; Alternative splicing.

Phosphorylation; Alternative splicing.

DNA_BIND 5 86

VARSPLIC 91 95 VAGCS -> SHCAP (IN ISOFORM 2).

VARSPLIC 96 428 MISSING (IN ISOFORM 2).
                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL; TISSUE-Embryo;
MEDLINE-97017146; PubMed-8863747;
Grevin D., Ung S., Denhez F., Deh
Stehelin D., Martin P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M25269; AAA52384.1; --
EMBL; AF080616; AAC82466.1; --
EMBL; AL009172; CAA15659.1; --
EMBL; AF000672; AAD00862.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T00250; -.
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                      TISSUE-Embryo;
MEDLINZ-95047310; PubMed-7958835;
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                              ELK1
                                                                                                                                                                                                                                                          ETS-DOMAIN
            Giovane A., Pintzas A., Maira
                                                    SEQUENCE OF 5-224
                                                                                Gene
                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                           "Structure and organization of
                                                                                                                                                                                                                                                                                                                                                                                             310
                                                                                                                                                                                                                                                                                                                                                                                                                     189 PQKGRKPR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: LUNG AND TESTIS PTM: PHOSPHORYLATED BY THE THREE GRO
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                                                                               174:185-188(1996).
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 new
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(Rel. 34, Last sequence update)
(Rel. 38, Last annotation update)
Pintzas A., Maira S.-M., Sobieszczuk P., ets transcription factor that is activate
                                                                                                                                                                                                                                                                                                                                                                                                                                               3.8%;
ilarity 100.0%;
Conservative
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                                                     FROM
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                                                                                                                                                                                                                                                          ELK-1.
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Pred. No
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S -> N (IN REF. 1).
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                                                                                          the mouse
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Matches 8
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15-DEC-1998;
15-DEC-1998;
01-OCT-2000;
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PROSITE; PS00345; ETS_DOMAIN...; 1.
PROSITE; PS00346; ETS_DOMAIN...; 1.
PROSITE; PS50061; ETS_DOMAIN...; 1.
Transcription regulation; Activato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; x87257; CAA60715.1; -. EMBL; z36939; CAA85391.1; -. HSSP; P14921; 2STW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PRO-NEUREGULIN-2 PRECURSOR (PRO-NRG2) [CONTAINS: NEUREGULIN-2 (NRG-2)
(NEURAL-AND THYMUS-DERIVED ACTIVATOR FOR ERBB KINASES) (NTAK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSD; P14921; 2STW.
MGD; MGI:101833; Elk1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                    MEDLINE=98006324; PubMed=9348101;
Higashiyama S., Horikawa M., Yama
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRG2_HUMAN
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MEDLINE=97342638;
                     TISSUE=Fetal brain;
                                           SEQUENCE FROM N.A. (ISOFORMS DON-18
                                                                                                             that
                                                                                                                                                                                                                                                       TISSUE=Neuroblastoma
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     NRG2 OR NTAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                     ishiguro H.;
novel brain-derived member
                                                                                                                                                                                      Nakagawa
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIVERGENT OF NEUREGULIN 1) (DON-1)]
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SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: PREDOMINAN
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FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
                                                                                       interacts with ErbB3 and ErbB4 iochem. 122:675-680(1997).
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8; Conser
                                                                                                                                                                                 T., Miyagawa J., Matsushita
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PubMed=9199335
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133
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0; Mismatches
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tsushita N.,
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B61B5B977731D54F
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                                                                                                                                   epidermal
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                                                DON-1R)
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Nagatsu T.
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Match Length DB
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213
    425026 segs, 132305027 residues
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sp_bacteria:*
sp_fungi:*
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sp_phage:*
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11 Q9EQQ1
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Q9HC30
 1 Q9EQQ1
Q9HVX4
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                                                                           O9ygd6 oncorhynchu
O9pt38 oncorhynchu
O9pt37 oncorhynchu
O9pt36 oncorhynchu
O9hc30 homo sapien
O9fh55 arabidopsis
O9gtj4 ancylostoma
O9u9k3 manduca sex
O9eqg1 cavia porce
O9i0c0 pseudomonas
O9hvx4 pseudomonas
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₹.	276 AA;	tase.	PRINTS; PRO0080; SDRFAMILY	PRINTS; PR00081; GDHRDH.	Pfam; PF00106; adh_short; 1.	InterPro; IPR002347;	InterPro; IPR002198;	HSSP; P50163; 2AE1.	EMBL; AF100930; AAD20217.1;		-!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)	Biochem. Biophys. Res. Commun. 255:123-128(1999).	trout (Oncorhynchus mykiss).";	hydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow	"Cloning and expression of two carbonyl reductase-like 20beta-	Tanaka	MEDLINE=99185307; PubMed=10082666;	SEQUENCE FROM N.A.		NCBI_TaxID=8022;	opteryq	Actinopterygii; Neopterygii; Teleostei; Euteleostei;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).				_		PRELI		
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01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-MAR 2010 (TrEMBLrel. 16, Last sequence update)
01-MAR 2010 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE,
Oncorniynchus mykiss (Rainbow trout) (Salmo gairdneri),
Eukaryota, Metazoa; Chordata; Craniata; Verrebrata; Eutactinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhy
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                  CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE ONCORPHYNCHUS mykiss (Rainbow trout) (Salmo gairdneri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhy NCBI_TaxID-8022;
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01-MAY-2000
                                             Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagaha McLoning and expression of two carbonyl reductase-like 20bets hydroxysteroid dehydrogenase CDNAs in ovarian follicles of ratrout (Oncorbynchus mykiss).";
Biochem. Biophys. Res. Commun. 255:123-128(1999).
-t- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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PRINTS; PR00080; SDRFAMILY.
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"Cloning and expression of two carbonyl reductase-like i
hydroxysteroid dehydrogenase cDNAs in ovarian follicles
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SEQUENCE 276
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Biochem. Biophys. Res. Commun. 255:123-128(1999).
-!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
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InterPro; IPR002198; -.
InterPro; IPR002347; -.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
Oxidoreductase.
SEQUENCE 276 AA; 30127 MW;
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01-MAY-2000
01-MAY-2000
01-MAR-2001
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                                                                   Q9HC30;
01-MAR-2001 (TIEMBLIEL. 16, Created)
01-MAR-2001 (TIEMBLIEL. 16, Last sequence update)
01-MAR-2001 (TIEMBLIEL. 16, Last annotation update)
01-MAR-2001 (TIEMBLIEL. 16, Last annotation update)
CAMP SPECIFIC PHOSPHODIESTERASE VARIANT PDE4A-10 (FRAGMENT)
  Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                            Q9HC30
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SEQUENCE 276 AA;
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Pfam; PF00106; adh_short; 1.
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Biochem. Biophys. Res. Commun. 255:123-128(1999).
-!- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
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                                                   PDE4A.
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PRINTS; PR00080; SDRFAMILY.
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8; Conserv
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  Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30139 MW;
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Last annotation updat
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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1: /SIDS8/acada+
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                                                                           : /SIDSB/gcgdata/geneseq/yeneseqp/AA1982.DAT: *
/SIDSB/gcgdata/geneseq/yeneseqp/AA1983.DAT: *
/SIDSB/gcgdata/geneseq/yeneseqp/AA1983.DAT: *
/SIDSB/gcgdata/geneseq/yeneseqp/AA1984.DAT: *
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/SIDSB/gcgdata/geneseq/geneseqp/AA1998.DAT: *
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
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SUMMARIES

Score	Match I	ength		ID	Description
213	100.0	213	21	AAY96431	Vervet TGF-beta bi
135	63.4	213	21	AAB26106	Human DAN/Cerberus
135	63.4	213	21	AAY96429	Human TGF-beta bin
135	63.4	213	22	AAY97589	Human secreted pro
115	54.0	176	21	AAY96434	Bovine TGF-beta bi
113	53.1	213	21	AAY96430	Human TGF-beta bin
113	53.1	213	21	AAY96436	Human TGF-beta bin
77	36.2	367	٤	AAB26105	Human DAN/Cerberus
33	15.5	50	20	AAY12009	Human 5' EST secre
33	15.5	213	21	AAY96433	Rat TGF-beta bindi
32	15.0	211	21	AAY96432	Murine TGF-beta bi
	Score 213 135 135 115 113 113 113 33 33 33	11 :		Match Length DB 100.0 213 21 163.4 213 21 63.4 213 21 63.4 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 55.5 213 21	Match Length DB 100.0 213 21 63.4 213 21 63.4 213 21 63.4 213 21 54.0 176 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 53.1 213 21 15.5 50 20 15.5 50 20 15.5 213 21 15.0 211 21

WPI; 2000-412321/35

ALIGNMENTS

RESULT AAY96431

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Vervet TGF-beta binding protein (BEER).
               Brunkow ME,
Van Ness J,
                                             (DARW-) DARWIN DISCOVERY LTD.
                                                                 27-NOV-1998;
                                                                                     24-NOV-1999;
                                                                                                       08-JUN-2000.
                                                                                                                           WO200032773-A1
                                                                                                                                            Cercopithecus pygerythrus.
                                                                                                                                                                osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                                                                                                                                                                                                               12-SEP-2000 (first entry)
                                                                                                                                                                                                                                       AAY96431;
                                                                                                                                                                                                                                                         AAY96431 standard; Protein; 213 AA
                Galas DJ,
Winkler DG;
                                                                 98US-0110283.
                                                                                     99WO-US27990.
                           Kovacevich B,
                          Mulligan JT,
                           Paeper BW;
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N-PSDB; AAA29057

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This shows a vervet transforming growth factor-beta (TGF-beta) binding protein designated VBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 122-123; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteoporosis and fractures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                          gene therapy
                                                                                                                                                                                                       Human; DNA/Cerberus-related protein 6; hDCR6; morphogenic protein;
antagonist; BMP; cell growth; cell differentiation; bone formation
                                                                                                                                                                                                                                                    Human DAN/Cerberus-related protein 6 (hDCR6) (exons 1 and 4).
                                                                                                                                                                                                                                                                                                                                                 AAB26106 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated with low mineral content.
                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                       15-JAN-2001
    (REGE-) REGENERON PHARM INC
                                  12-MAR-1999;
                                                                02-MAR-2000;
                                                                                                21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFGPEAARPQKGRKPRPRARGAKANQAELENAY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGKWWRPSGPDFRCIPDRYRAQRVQLLCPGGAAPRARKVRLVASCKCKRLTRFHNQSELK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                2000WO-US05537
                                                                                                                                                                                                                                                                                    (first entry)
                                 99US-0124118
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Pred. No. 4.3e-214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                            bone formation;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence comprises the amino acid sequence encoded by exons and 4 of the human DAN/Cerberus-related protein 6 (hDCR6) coding sequence. The coding sequence was isolated from a human kidnay cDNA library containing exons 1 and 4 of the sequence. HDCR6 is closely related to the DAN and DCR5 proteins, both of which act as antagonists morphogenic proteins such as BMP. It is possible that the hDCR6 gene an protein can be used as immunogens, modulators of cell function, growth and differentiation, to reduce undesirable bone formation, to identify DCR6 binding agents, in diagnosis, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated, human DNA/Cerberus related protein 6 which include natural homologue, and polypeptides comprising DCR6 domain and nucleic acids encoding the proteins which are useful as probes and primers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                          osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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              N-PSDB; AAA29055
                                                                                                                                        24-NOV-1999;
                                                                                                                                                                08-JUN-2000
                                                                                                                                                                                        WO200032773-A1
                                                                                                                                                                                                                                         BEER;
                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                      12-SEP-2000
                                                                                                                                                                                                                                                                                                                              AAY96429;
                                                                                                                                                                                                                                                                                                                                                    AAY96429 standard;
                          WPI; 2000-412321/35
                                                              Brunkow ME,
                                                                                                                                                                                                                 Homo sapiens
                                                                                       (DARW-) DARWIN DISCOVERY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                    137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt afrvvegqgwqafkndatelipelgeypeppelennktmnraenggrpphhpfetkdvs}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135;
                                                                                                                                                                                                                                                                             TGF-beta binding protein (BEER).
                                                                                                                                                                                                                                        gene therapy;
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                                                   Winkler
                                                              Galas DJ,
                                                                                                                98US-0110283
                                                                                                                                        99WO-US27990
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                                                   DG;
                                                               Kovacevich
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Pred. No. 9.7e-133;
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Title:
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein search, using sw model
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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         ВB
US-08-468-847B-2
US-09-188-930-159
US-09-188-930-286
US-09-189-930-286
US-09-398-496-32
US-08-484-905-61
US-08-370-476-61
US-08-370-476-61
US-08-382-298-15
US-08-475-316A-13
US-08-98-15
US-08-588-983-16
US-08-588-983-16
US-08-588-983-16
US-08-588-976-16
US-08-588-976-16
US-08-588-976-16
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US-08-690-011A-31
US-08-690-011A-31
US-08-690-011A-31
US-08-690-011A-31
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US-08-690-93A-30
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100.571 Million cell updates/sec
Sequence 2, Appli Sequence 159, App Sequence 286, App Sequence 32, Appli Sequence 61, Appli Sequence 15, Appli Sequence 15, Appli Sequence 17, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 15, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 30, Appli Sequence 20, Appli Sequence 20, Appli Sequence 30, Appli Sequence 20, App
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Sequence 2, Application US/08468847B Patent No. 5780263 REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2: COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,84 SEQUENCE CHARACTERISTICS: LENGTH: 206 AMINO ACID TYPE: AMINO ACID FILING DATE: 6 June 1 CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD TOPOLOGY: L: MOLECULE TYPE: ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33, APPLICANT: Hastings, TITLE OF INVENTION: 1 NUMBER OF SEQUENCES: STRANDEDNESS: FILING DATE: CITY: ROSELAND STATE: NEW JERS INFORMATION: : 206 AMINO ACIDS AMINO ACID NEW JERSEY 6 June 1995 N: 435 Human CCN-Like Growth Factor 20 US/08/468,847B 33,073 325800-442

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RESULT 2
US-08-468-847B-20
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Best Local s
Matches s
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MOLECULE TYPE:
S-08-468-847B-20
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                                                                               GENERAL INFORMATION:
                                                                                             Sequence 159, Application US/09188930A Patent No. 6150502
                                                                                                                                                                                                                                                                              Query Match
Best Local
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TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                Matches
            APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION UNBER: US/08/46:
FILING DATE: 6 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
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NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32.0
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                                                                                                                                                                                                                                                              Local Similarity hes 9; Conserv
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OPERATING SYSTEM:
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STATE: NEW JERSEY
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9; Conservative
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E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
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James Greg
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100.0%; Pr
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; Pred. No.
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No. 0.37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-159
                                                                                                                                                                                              US-08-753-007A-32

Sequence 32, Application US/08753007A

Patent No. 6074841

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 159
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6150502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compositions Isolated From TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011c1
                                                             TITLE OF INVENTION: DON-1 GENE
TITLE OF INVENTION: AND USES TH
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                               APPLICANT: Gearing, David P. APPLICANT: Busfield, Samanth
                                                                                                                                                                                                                                                                                                                                               28 AFKNDATEI 36
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 COUNTRY: US
ZIP: 02110-2804
                                   STATE:
                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286,
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                                                                                                                                                DON-1 GENE AND POLYPEPTIDES
                                                                               Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No.
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5. 0.37;
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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	hypothetical prote	myosin heavy chain	cell surface glyco		outer membrane hem	surface glycoprote	probable cysG prot			hypothetical prote	dipeptide transpor	nic dipep	probable binding p	polyferredoxin 6x2	hypothetical prote	hypothetical prote		-type pl			g		-		hypothetical prote	- 1		nsforming pro	Description

ALIGNMENTS

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RESULT 2
JC4965
elkl protein - mouse
cl. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999
C. Accession: JC4965; I48339; I48340; S54908
R:Grevin, D.; Ung, S.; Denhez, F.; Dehem, M.; Quatannens, B.; Begue, A.; Stehelin, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Gene: GDB:ELK1
A.Gross-references: GDB:119867; OMIM:311040
A.Map position: Xp11.2-Xp11.2
C.Superfamily: elk-1 transforming protein; ets DNA-binding domain homology C:Keywords: DNA binding; oncogene; transforming protein F:7-86/Domain: ets DNA-binding domain homology <ETS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M25269; NID:g538208; PIDN:AAA52384.1; PID:g538209 R;Gille, H.; Kortenjann, M.; Thomae, O.; Moomaw, C.; Slaughter, C.; Cobb, EMBO J. 14, 951-962, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: elk, tissue-specific ets-related genes on chromosomes X and 14 near transloc A;Reference number: A41354; MUID:89203250 A;Accession: A41354
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C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A41354; S54721
C;Accession: A41354; S54721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Rao, V.N.; Huebner, K.; Isobe, M.; ar-Rushdi, A.; Croce, C.M.; Reddy, E.S.P. Science 244, 66-70, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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A; Residues: 1-428 < RAO>
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Best Local :
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R:Glovane, A.; Pintzas, A.; Maira, S.M.; Sobieszczuk, P.; Wasylyk, B. Genes Dev. 8, 1502-1513, 1994
A;Title: Net, a new ets transcription factor that is activated by Ras A;Reference number: A53837; MUID:95047310
A;Accession: I48339
RESULT
D83305
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A; Molecule type: protein
A; Residues: 1-99 <WOL>
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                                                                                                                                                                                                                                                                                                           A;Description: necessary for the expression of MHC class I histocysuperfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterodimer E:18-82/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                              C; Complex: heterodimer with MHC class I histocompatibility antigen alpha chain C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wolfe, P.B.; Cebra, J.J.
Mol. Immunol. 17, 1493-1505, 1980
A;Title: The primary structure of guinea
A;Reference number: A02181; MUID:82057805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-2-microglobulin - guinea pig
N;Alternate names: class I histocompatibility antigen beta chain
C:Species: Cavia porcellus (guinea pig)
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A;Introns: 70/3; 219/3; 363/3; 397/3
A;Introns: 70/3; 219/3; 363/3; 397/3
C;Superfamily: elk-1 transforming protein; ets DNA-binding F;7-86/Domain: ets DNA-binding domain homology <FTS>
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A; Title: Structure and
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Best Local Similarity
"hes 7; Conserva
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C:Accession: A02181
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A; Residues: 1-429 < RES>
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A; Residues: 1-429 < GRE>
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A; Residues: 5-132, 'T', 134-224 <RE2>
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Matches 8; Conser
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de bonds: #status predicted
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A;Molecule type: DNA
A;Residues: 1-148 <STO>
A;Cross-references: GB:AE004858; GB:AE004091; NID:g9950668; PIDN:AAG07829.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA4441 [imported] - Pseudomona C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: D83305
                                                                                                                         C; Genetics:
A; Gene: PA4
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                                                                                                                                                                                                                                                                                A; Title: Complete genome
                                                                                                                                                                                                                                                                                                 .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A;Experimental source: strain PAO1
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A; Residues: 1-130 <STO>
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Matches 7
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110 ARLLPNA 116
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                                    Similarity 7; Conserv
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100.0%; Pr
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100.0%; Pr
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Pred. No.
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r, S.N.; Fo
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A.; Larbig,
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A.; Larbig, K.; L
                                        Gaps
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R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eise, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vzmathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authbors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, A;Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain MCI A;Reference number: A81000; MUID:20175755

Dougherty, Pizza, M.

MC58.

Eisen,

serogro

hypothetical protein NMB1656 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

G81057

RESULT

C; Accession: G81057

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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKV; ARE
                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A. MEDINE-89203250; PubMed=2539641; MEDLINE-89203250; PubMed=2539641; Rao V.N., Huebner K., Isobe M., Ar-Rushdi A., Croce C.M., Reddy E.S.P.; Pubmer K., Isobe M., Ar-Rushdi A., Croce C.M., reddy E.S.P.; Pubmer K., Isobe M., Ar-Rushdi A., Croce C.M., reddy E.S.P.; State-specific ets-related genes on chromosomes X and 14 near translocation breakpoints."; Science 244:66-70(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
Aryee D.N.T., KOVAZ H.;
Novel family members HuER71, ELFR, and ELKv among ETS-related genes coexpressed with EWS-FIII in Ewing tumor cell lines.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99013876; PubMed=9795224;
MEDLINE=99013876; PubMed=9795224;
Malls F.C., Mills F.C., Mitchell M.P., Meindl A., Max E.E.;
"The human ell-1 gene family: the functional gene and two processed pseudogenes embedded in the IgH locus.";
Gene 221:215-224(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                        Grafham D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                            ELK1.HUMAN STANDARD; PRT; 428 AA. P19419; 075606; Q9UJM4; 095058; 01-007-1200 (Rel. 16, Created) 01-007-2000 (Rel. 40, Last sequence update) 01-007-2000 (Rel. 40, Last sequence update) ELS-DOMAIN PROTEIN ELK-1.
                                                                                                                                                                       ALIGNMENTS
                 FGFH_MOUSE
PRL_HUMAN
PRL_MACMU
COX2_BRAFL
COX2_BRAFL
DAPB_MYCTU
                                                                                        LEF5_NPVOP
DAPB_BACSU
ESL1_MYCPN
THIM_BACSU
HES1_HUMAN
                                                                     APX1_PEA
DHSB_RICPR
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NCBI_TaxID=9606;
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1 MQPSLAPCLICLLVHAAFCA......KPRPGARGAKANQAELENAY 211
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                          2001, 15:47:56
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REV_HV1LW
RL22_PHYS1
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ELK1_MOUSE
VE7_HPV44
B2MG_CAVPO
RL22_LEPIN
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DPPA_ECOLI
VGLG_SYNV
CSG_HALHA
MXSC_ACACA
MXSC_ACACA
ILHA1_RHOAC
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RL12_ECOLI
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HS72_CANAL
RETB_CHICK
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Phosphorylation.
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CONFLICT 133
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Q80914;
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                     -1- TISSUE SPECIFICITY: LUNG AND TESTIS.-1- PIM: PHOSPHORYLATED BY THE THREE GROUPS OF MAP KINASE (P38, JNK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000418; -.
Pfam: PF00178; Ets; 1.
PRINTS: PR00454; ETS.DOMAIN.
PROSITE: PS00346; ETS.DOMAIN.]; 1.
PROSITE: PS50061; ETS.DOMAIN.]; 1.
PADSPHOTYJALION; ALTERNATIVE SPLICING.
PADSPHOTYJALION; ALTERNATIVE SPLICING.
PADSPHOTYJALION; ALTERNATIVE SPLICING.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grevin D., Ung S., Denhez F., Dehem M., Quatannens B., Begue A., Stehelin D., Martin P.; Structure and organization of the mouse elk1 gene."; Gene 174:185-188(1996).
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MISSING (IN ISOFORM 2).
S -> N (IN REF. 1).
68F71F8ADB9D38CA CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.8%; Score 8; DB 1
100.0%; Pred. No. 1;
Live 0; Mismatches
                                                                                    -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
  PRODUCED BY ALTERNATIVE SPLICING
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MEDLINE=95047310; PubMed=7958835;
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STRAIN-C57BL; TISSUE-Embryo;
MEDLINE-97017146; Pubmed-8863747;
                                                                                                                                                                                                                                                                                                                           EMBL; AF080616; AAC82466.1; -. EMBL; AL009172; CAA15659.1; -. EMBL; AF000672; AAD00862.1; -.
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Best Local Similarity 100.
Matches 8; Conservative
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428
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HSSP, P14921; 2STW.
TRANSFAC; T00250; -.
MIM; 311040; -.
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428 AA;
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P41969;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                               -:- SUBCELLULAR LOCATION: NUCLEAR.
-:- TISSIE SPECIFICITY: PREDMINANTLY EXPRESSED IN THE BRAIN, AND TO
LESSER EXTERT IN THE HEART, LIVER AND MUSCLE.
-:- SIMILARITY: BELONGS TO THE ETS FAMILY.
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Submitted (ocr-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 44.
Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
NCBL_TaxID=10592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes Dev. 8:1502-1513(1994).
-i- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA
SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE
FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE
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B61B5B977731D54F CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
E7 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 AA.
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InterPro; IPR000148; -.
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Best Local Similarity
Matches 8; Conserv
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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                     Score
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
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Match Length DB
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1 MQPSLAPCLICLLVI
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sp_phage:*
sp_plant:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
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sp_bacteria:*
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O9fh55 arabidopsis
O9gtj4 ancylostoma
O9eqd1 cavia porce
O9i0C0 pseudomonas
O9i0C0 pseudomonas
O9iyb9 neisseria m
O9jta0 neisseria m
O9jta0 neisseria m
O9jta0 neisseria m
O9jta0 streptomyce
O9ibj1 turkey herp
O9ibj1 turkey herp
O9ibj2 streptomyce
O9xf19 arabidopsis
O9xf19 arabidopsis
O9xf19 rabidopsis
O9pf72 ureaplasma
O9r119 cricetulus
O35771 rattus norv
O9fun1 zea mays (m
O9i5y7 pseudomonas
O9rjx3 streptomyce
O91g89 oryza sativ
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ALIGNMENTS

RESULT

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
2INC METALLOEPETIDASE 3 MED3 (FRAGMENT)
Ancylostoma caninum (Dog hookworm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatoidea; Ancylostomatoidea; Ancylostomatoidea; NCBI_TaxID-29170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10141;
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Q9EQQ1; 17EMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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"Cloning and characterization of a zinc-metalloprotease secreted the invasive stages of Ancylostoma caninum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF273706; AAG29106.1; -.
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SEQUENCE 125 AA; 13977 MW; 3F3224B02F0B41C
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                                    Bacteria; Proteobacteria;
                                                                        Pseudomonas aeruginosa
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Local Similarity 100.0%;
hes 7; Conservative
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Q9HVX4;
Q9HVX4;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, I
01-MAR-2001 (TrEMBLrel. 16, I
HYPOTHETICAL PROTEIN PA4441.
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Q9JYB9
Q9JYB9;
01-OCT-2000
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                                                                                                                                                                                                                                                                                   MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warrener P., Hickey M.J. Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Lorbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen IT., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                               "Complete genome sequence of Pseudomonas aeruginosa PA01, opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004858; AAG07829.1;
                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 148 AA; 16418
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
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130 AA; 14
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Pred. No. 17;
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8 3.8 428 20 AAY52704 8 3.8 428 20 AAY52704 8 3.8 481 21 AAG34091 8 3.8 490 21 AAG34091 8 3.8 490 21 AAG34099 8 3.8 512 21 AAG34099 7 3.3 95 21 AAR47202 7 3.3 99 21 AAY52883 7 3.3 99 21 AAY52883 7 3.3 99 22 AAB58644 7 3.3 99 22 AAB58644 7 3.3 265 21 AAG42285 7 3.3 265 21 AAG42286 7 3.3 265 21 AAG42284 A 3.3 265 21 AAG47031 A 3.4 21 AAG47031 A 4 3 1	secrete		20	41		σ	42
8 3.8 428 20 AAY52704 8 3.8 428 20 AAY52704 8 3.8 481 21 AAG34091 8 3.8 481 21 AAG34091 8 3.8 490 21 AAG34099 8 3.8 512 21 AAG34099 8 3.8 512 21 AAG34099 7 3.3 95 21 AAY58229 7 3.3 99 21 AAY58229 7 3.3 99 21 AAY58229 7 3.3 99 21 AAY68229 7 3.3 99 21 AAG42285 7 3.3 201 12 AAG10425 7 3.3 205 21 AAG42284 7 3.3 265 21 AAG42284 7 3.3 265 21 AAG42283 7 3.3 265 21 AAG42284 7 3.3 265 21 AAG42283 7 3.3 265 21 AAG42284 A AAG47030 A AAG4			22	22		6	41
8 3.8 428 20 AAY52704 8 3.8 428 20 AAY52704 8 3.8 481 21 AAG34091 8 3.8 481 21 AAG34091 8 3.8 490 21 AAG34091 7 3.3 86 15 AAR47202 7 3.3 99 21 AAY58289 7 3.3 99 21 AAY58289 7 3.3 99 22 AAB58644 7 3.3 265 21 AAG42285 7 3.3 265 21 AAG42285 7 3.3 265 21 AAG42286 7 3.3 265 21 AAG42288 7 3.3 265 21 AAG47030 7 3.3 265 21 AAG47031 7 3.3 431 21 AAG47031 7 3.3 500 21 AAG47030 8 AAW40710 8 AAW40710 8 AAW40710 9 APP1ide 6 2.8 10 18 AAW40711 6 2.8 10 18 AAW40712 6 2.8 12 10 AAP50474 Human pr Sequence bcl-x(t) Peptide peptide peptide Sequence bcl-x(t)	N-terminal pro		13	20		6	10
8 3.8 428 20 AAY52704 8 3.8 428 20 AAY32824 8 3.8 481 21 AAG34091 8 3.8 481 21 AAG34091 8 3.8 490 21 AAG34090 7 3.3 92 21 AAY58283 7 3.3 99 22 AAB58644 7 3.3 99 22 AAB58644 7 3.3 265 21 AAG22845 7 3.3 265 21 AAG22845 7 3.3 265 21 AAG47232 7 3.3 265 21 AAG47233 7 3.3 265 21 AAG47233 8 431 21 AAG477331 8 AAG477331 AAAG477331 AAAG			19	15		O	39
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52824 Human ELK-1 8 3.8 428 20 AAY32824 Human ELK-1 8 3.8 428 20 AAY32824 Zea mays pro 8 3.8 490 21 AAG34091 Zea mays pro 9 21 AAG34099 Zea mays pro 9 21 AAF57202 Immunostimul 7 3.3 99 21 AAY52883 Guinea pig b 7 3.3 99 21 AAY52883 Guinea pig b 7 3.3 99 21 AAY52883 Guinea pig b 7 3.3 201 12 AAR10425 Arabidopsis 7 3.3 201 12 AAR10425 Arabidopsis 7 3.3 265 21 AAG47284 Arabidopsis 7 3.3 265 21 AAG47284 Arabidopsis 7 3.3 282 21 AAG47284 Arabidopsis 7 3.3 265 21 AAG47031 Arabidopsis 7 3.3 265 21 AAG47030 Arabidopsis 6 2.8 10 18 AAW40710 Peptide whic 6 2.8 10 18 AAW40711 Peptide whic 6 2.8 10 18 AAW40711 Peptide whic 6 2.8 10 18 AAW40711 Peptide whic 6 2.8 11 01 AAW40711 Peptide whic 6 2.8 12 0 AAP50474 Human prolac 6 2.8 13 7 AAF05742 Sequence from 6 2.8 14 17 AAR55155 bcl-x(L)/bcl			19	15		σ	38
## 8 3.8 428 20 AAY52704 Human ELK-1 ## 8 3.8 428 20 AAY52704 Human ELK-1 ## 8 3.8 481 21 AAG34091 Zea mays pro	$\overline{}$	AAR9515	17	14		0	37
## 8 3.8 428 20 AAY52704 Human ELK-1 ## 8 3.8 428 20 AAY52704 Human ELK-1 ## 8 3.8 481 21 AAG34091 Zea mays pro			7	13		6	36
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34091 Zea mays pro 8 3.8 512 21 AAG34090 Zea mays pro 8 3.8 512 21 AAG34089 Immunostimul 7 3.3 86 15 AAR47202 Guinea pig b 7 3.3 99 21 AAY58229 Guinea pig b 7 3.3 99 21 AAY58288 Guinea pig b 7 3.3 99 21 AAY68229 7 3.3 201 12 AAR10425 Arabidopsis 7 3.3 265 21 AAG42284 Arabidopsis 7 3.3 265 21 AAG472284 Arabidopsis 7 3.3 265 21 AAG47284 Arabidopsis 8 3.8 481 21 AAG47030 Arabidopsis 9 3.3 501 21 AAG47030 Arabidopsis 9 3.3 511 21 AAG47030 Arabidopsis 9 2.8 10 18 AAW40710 Peptide whic 1 2 8 10 18 AAW40711 Peptide whic 1 2 AAF50474 Determinant s	Human prolacti		10	12		σ	5
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8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 8 3.8 490 21 AAG34090 8 3.8 490 21 AAG34090 7 3.3 23 15 AAR57116 Immunostimul 7 3.3 99 21 AAY52883 Guinea pig b 7 3.3 99 21 AAY52883 Guinea pig b 7 3.3 201 12 AAG42285 Arabidopsis 7 3.3 219 21 AAG42286 Arabidopsis 7 3.3 265 21 AAG42286 Arabidopsis 7 3.3 431 21 AAG47031 Arabidopsis 7 3.3 510 12 AAG47031 Arabidopsis 8 2.8 10 18 AAW40700 Peptide whic 10 18 AAW40711 Peptide whic			18	10		6	ω
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 8 3.8 512 21 AAG34089 Zea mays pro 9 21 AAY52089 Immunostimul 7 3.3 96 15 AAR57202 Immunostimul 7 3.3 99 21 AAY68229 Guinea pig b 9 21 AAY52883 Guinea pig b 9 21 AAY52883 Guinea pig b 9 21 AAY68229 Guinea pig b 9 21 AAY68229 AAB58644 E.coli fpp g 9 3.3 201 12 AAR10425 Arabidopsis 9 3.3 265 21 AAG42284 Arabidopsis 9 3.3 282 21 AAG47030 Arabidopsis 9 3.3 500 21 AAG47030 Arabidopsis 9 3.3 511 21 AAG47029 Arabidopsis 9 3.4 11 21 AAG47029 Arabidopsis 9 3.8 10 18 AAM40709 Peptide whic			18	10		σ	32
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 7 3.3 51 21 AAG34090 Zea mays pro 7 3.3 86 15 AAR7116 Immunostimul 7 3.3 99 21 AAY68229 Guinea pig b 7 3.3 99 21 AAY68229 Guinea pig b 7 3.3 99 21 AAF28283 Guinea pig b 7 3.3 29 22 AAB58644 E.coli fip g 7 3.3 21 AAG42284 Arabidopsis 7 3.3 21 AAG47283 Arabidopsis 7 3.3 25 21 AAG47033 Arabidopsis 7 3.3 31 21 AAG47033 Arabidopsis 7 3.3 50 <t< td=""><td></td><td></td><td>18</td><td>10</td><td></td><td>6</td><td>31</td></t<>			18	10		6	31
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 9 21 AAG34090 Zea mays pro 1 3.3 23 15 AAR57116 Immunostimul 1 3.3 99 21 AAY52883 Guinea pig b 1 3.3 99 21 AAY52883 Guinea pig b 1 3.3 201 12 AAR4042285 Arabidopsis 1 3.3 265 21 AAG42284 Arabidopsis 1 3.3 431 21 AAG47031 Arabidopsis 1 3.3 510 21 AAG47030 Arabidopsis 1 3.3 511 21 AAG47026 Human ventris			18	10		6	30
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34091 Zea mays pro 8 3.8 512 21 AAG34090 Zea mays pro 7 3.3 86 15 AAR57116 Immunostimul. 7 3.3 99 21 AAY68229 Guinea pig b 7 3.3 99 21 AAY68229 Guinea pig b 7 3.3 99 21 AAY68229 7 3.3 99 22 AAB58644 Guinea pig b 7 3.3 201 12 AAR10425 E.coli fpp g 7 3.3 265 21 AAG42284 Arabidopsis 7 3.3 282 21 AAG47031 Arabidopsis 7 3.3 500 21 AAG47039 Arabidopsis			12	10		6	29
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 9 3.8 512 21 AAG34090 Zea mays pro 1 3.3 23 15 AAR57116 Immunostimul 1 3.3 99 21 AAY68229 Guinea pig b 1 3.3 99 21 AAY68229 Guinea pig b 2 3.3 99 21 AAY52883 Guinea pig b 2 3.3 99 21 AAY68229 Guinea pig b 3 3.3 20 21 AAA642283 Guinea pig b 3 3.3 219 21 AAA642284 Arabidopsis 3 3.3 285 21 AAG42284 Arabidopsis 3 3.3 281 21 AAG47030 Arabidopsis			21	511	٠	7	28
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34091 Zea mays pro 9 21 AAG34090 Zea mays pro 1 3.3 23 15 AAR57116 Immunostimul 1 3.3 86 15 AAR47202 Immunostimul 1 3.3 99 21 AAY68229 Guinea pig b 1 3.3 99 21 AAY52883 Guinea pig b 1 3.3 201 12 AAR410425 E.Coli fpg g 1 3.3 202 21 AAG42284 Arabidopsis 1 3.3 282 21 AAG47031 Arabidopsis			21	500	٠	7	27
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 8 3.8 481 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 7 3.3 85 12 21 AAG34089 Immunostimul. 7 3.3 96 15 AAR47202 Immunostimul. 7 3.3 99 21 AAY68229 Guinea pig b 7 3.3 201 12 AAR10425 Guinea pig b 7 3.3 201 12 AAR10425 AAR10425 7 3.3 265 21 AAG42284 Arabidopsis			21	431		7	95
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 8 3.8 428 20 AAY32824 8 3.8 428 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 9 21 AAG34090 Zea mays pro 1 3.3 23 15 AAR57116 Immunostimul 1 3.3 46 15 AAR47202 Guinea pig b 1 3.3 99 21 AAY5829 Guinea pig b 1 3.3 99 21 AAY5829 Guinea pig b 1 3.3 99 21 AAY5829 Guinea pig b 2 3.3 201 12 AAR10425 Ecoli fip g 2 3.3 201 12 AAR10425 Arabidopsis 2 3.3 265 21 AAG42284 Arabidopsis			21	282		7	Ğ
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY2824 Human ELK-1 8 3.8 428 20 AAY2824 8 3.8 428 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 9 21 AAG34090 Zea mays pro 1 3.3 23 15 AAR67116 Immunostimul 1 7 3.3 86 15 AAR47202 Immunostimul 2 7 3.3 99 21 AAY58229 Guinea pig b 2 7 3.3 99 21 AAY28283 Guinea pig b 3 3.3 99 22 AAR10425 E.coli figs 7 3.3 219 21 AAG42285 Arabidopsis			21	265		7	24
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 8 3.8 428 20 AAY32824 8 3.8 428 20 AAY32824 8 3.8 420 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 9 3.8 512 21 AAG34089 Zea mays pro 1 3.3 21 5 AAR57116 Immunostimul 1 7 3.3 99 21 AAY58229 Guinea pig b 1 3.3 99 21 AAY58283 Guinea pig b 2 3.3 99 22 AAB58644 Guinea pig b 3 3.3 201 12 AAR10425 E.coli fpp g			21	219		7	23
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY2824 8 3.8 428 20 AAY32824 8 3.8 428 20 AAY32824 8 3.8 429 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 9 21 AAG34090 Zea mays pro 1 3.3 23 15 AAR57116 Immunostimul 1 7 3.3 86 15 AAR47202 Immunostimul 2 7 3.3 99 21 AAY58829 2 7 3.3 99 21 AAY58829 3 3.3 99 21 AAY58864 3 Guinea pig b 3 Guinea pig b	ddj		12	201		7	22
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY52824 Human ELK-1 8 3.8 428 20 AAS23824 Human ELK-1 8 3.8 428 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 9 21 AAG34090 Zea mays pro 1 3.3 23 15 AAR57116 Immunostimul 1 7 3.3 86 15 AAR47202 Immunostimul 2 7 3.3 99 21 AAY52823 Guinea pig B 2 7 3.3 99 21 AAY52833 Guinea pig B	piq		22	99	٠	7	21
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 8 3.8 428 20 AAY32824 8 3.8 428 20 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 7 3.3 23 15 AAR47202 Immunostimul 7 3.3 99 21 AAY48229 Guinea pig b	pig		21	99		7	20
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 Human ELK-1 8 3.8 428 20 AAY32824 8 3.8 429 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 8 3.8 512 21 AAG34089 Zea mays pro 7 3.3 85 512 21 AAR57116 Immunostimul 7 3.3 86 15 AAR47202 Immunostimul	Guinea pig bet		21	99		7	[9
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 Human ELK-1. 8 3.8 428 21 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro 8 3.8 512 21 AAG34089 Zea mays pro 7 3.3 23 15 AAR57116 Immunostimul	Immunostimulai		15	86	٠	7	18
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 Human ELK-1 8 3.8 428 20 AAX32824 8 3.8 429 21 AAG34090 Zea mays pro 8 3.8 490 21 AAG34089 Zea mays pro	Immunostimulat	AAR5	15	23	٠	7	17
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 Human ELK-1 8 3.8 428 12 AAG34091 Zea mays pro 8 3.8 490 21 AAG34090 Zea mays pro	Zea mays prote		21	512		œ	9
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 Human ELK-1. 8 3.8 481 21 AAG34091 Zea mays pro	mays	AAG3409	21	490	٠	80	5
8 3.8 428 20 AAY52704 Human ELK-1 8 3.8 428 20 AAY32824 Human ELK-1.	mays		21	481		œ	14
8 3.8 428 20 AAY52704 Human ELK-1	ELK-1.		20	428		œ	
	ELK-1	AAY52704	20	428	3.8	œ	12

AAY96432 RESULT

μ

AAY96432 standard; Protein;

211 AA

Murine TGF-beta binding protein (BEER).

12-SEP-2000 (first entry)

AAY96432;

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WPI; 2000-412321/35
               Brunkow ME,
Van Ness J,
                                                          27-NOV-1998;
                                                                           24-NOV-1999;
                                                                                            08-JUN-2000.
                                                                                                                                              osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                                         (DARW-) DARWIN DISCOVERY LTD
                                                                                                             WO200032773-A1
                                                                                                                               Mus musculus.
               Galas DJ,
Winkler DG;
                                                          98US-0110283
                                                                            99WO-US27990
                        Kovacevich B,
                        Mulligan JT,
                        Paeper BW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                           , 27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This shows a murine transforming growth factor-beta (TGF-beta) binding protein designated mBEER. The cDNA and protein may be used for prevention, treatment and diagnossis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TCF-beta BP expression. The cDNA of the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                       AAY96433 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 124; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA29058
                                                                                              24-NOV-1999;
                                                                                                                                08-JUN-2000
                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                           osteopathic;
                                                                                                                                                                                                                                                                                              Rat TGF-beta
                                                                                                                                                                                                                                                                                                                                  12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                     AAY96433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated with low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoporosis and fractures
                     (DARW-) DARWIN DISCOVERY LTD
                                                                                                                                                                   WO200032773-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRPPHHPYDAKDVSEYSCRELHYTRFLTDGPCRSAKPVTELVCSGQCGPARLLPNAIGRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KWWRPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHNQSELKDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mqpslapclicllvhaafcavegqgwqafrndatevipglgeypepppennqtmnraeng 60
                                                                                                                                                                                                                                        therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                    transforming growth factor-beta; TGF-beta; binding protein; herapy; antisense therapy; fracture; bone mineralization.
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                          binding protein
                                                         98US-0110283.
                                                                                              99WO-US27990
                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mineral content.
                                                                                                                                                                                                                                                                                                                                                                                                       213
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                                                                                                                                                                                                                                                                                              (BEER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 211; DB 21;
Pred. No. 2.3e-210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
   WPI; 2000-412321/35
                                      Brunkow ME,
Van Ness J,
                                                                                          (DARW-) DARWIN DISCOVERY LTD
                                                                                                                              27-NOV-1998;
                                                                                                                                                                   24-NOV-1999;
                                                                                                                                                                                                       08-JUN-2000
                                                                                                                                                                                                                                          WO200032773-A1
                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96434 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoporosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunkow ME,
Van Ness J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                        Galas DJ,
Winkler DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galas DJ,
Winkler DG;
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                              98US-0110283
                                                                                                                                                                   99WO-US27990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fractures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
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inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The CDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for diagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders associated with low mineral content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rnis snows a rat transforming growth factor-beta (TGF-beta) protein designated rBEER. The cDNA and protein may be used prevention, treatment and diagnosis of diseases associated inanaromiliate names according
                                                                                                                                                                                                                                                                                                                                                                                                                            BEER; gene therapy; antisense therapy; fracture; bone mineralization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine TGF-beta binding protein (BEER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 125-126; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids (I) encoding a transforming growth factor beta be protein, useful for identifying agents for treating osteopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDGPCRSAKPYTELVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tdgpcrsakpvtelvcsgqcgparllpnaigrvkwwrpngpdfrcipdryraqrvqllcp
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Kovacevich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB 21;
Pred. No. 9.6e-104;
0; Mismatches 0;
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В,
Mulligan
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   JT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paeper BW;
Paeper BW;
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Title:
Perfect score:
Sequence:
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 50 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq
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     length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                       Match
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211
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
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US-08-250-789A-97
US-08-250-789A-97
US-08-661-479-18
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US-08-905-223-40
US-08-905-23-46
US-08-905-23-685-68
PCT-US95-11934-68
PCT-US95-11934-68
PCT-US95-11934-68
US-08-282-197C-44
US-08-836-791-5
US-08-666-798-2
US-08-985-526-25
US-08-985-671-2
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US-08-987-5316A-13
US-08-387-348-7
US-08-387-348-7
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Sequence 61, Appl
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Sequence 94, Appl
Sequence 95, Appl
Sequence 97, Appl
Sequence 18, Appl
Sequence 100, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 30, Appl
Sequence 27, Appli
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sequence 1, Appil	, 0	Sequence 6, Appli	Sequence 6, Appli	•	Sequence 1, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 278, App	Sequence 144, App	Sequence 2, Appli	Sequence 33, Appl	Sequence 27, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 3, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 3, Appli	Sequence 14, Appl	Sequence 13, Appl	Sequence 12, Appl	Sequence 1, Appli

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US-08-484-905-61
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Patent No.
                                                                                                                                                                      APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
CLASSIFICATION: 530
PRIOR APPLICATION: 530
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TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: POTTET, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 034
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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CITY: Washington
STATE: D.C.
ZIP: 20005-3315
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5. 5976551
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1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mottez, Estelle
Abastado, Jean-Pierre
Kourilsky, Philippe
VENTION: An Altered Major Histocompatibility
VENTION: Complex(MHC) Determinant and Methods
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                     61:
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Query Match
Best Local Similarity
Watches 7; Conserva
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                                                                                                                                                                                                        ; TOPOLOGY: 11; MOLECULE TYPE: US-08-481-9858-61
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GENERAL INFORMATION:
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TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC -DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/801,818
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PC-POS/MS-DOS

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APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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*TP: 20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 05-DEC-1991 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 15-NOV-1991
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                                                                                                                                                                                                                                                                                    amino acid
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amino acid
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1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                     99 amino acids
                                                                         3.3%; Score 7; DB ilarity 100.0%; Pred. No. 12
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Kenneth J. 25,146
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o. 12;
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RESULT 4
US-08-250-789A-94
: Sequence 94, Application US/08250789A
: Patent No. 5635597
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Best Local Similarity
Watches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-370-476-61
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Patent No. 6153408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
ADDITATION NUMBER: US 07/702,473
ADDITATION NUMBER: US 07/702,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CITY: Washington
STATE: D.C.
ZIP: 20005-3315
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CLASSIFICATION: 435
                                                                                                                                                        64 LLVHAAF 70
                                                                                                                                                                                                   12 LLVHAAF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/792,473
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Abastado, Jean-Pierre
                                                                                                                                                                                                                                                    3.3%; Score 7; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lone, Yu-Chun
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Result
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length: 2000000000
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213
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Copyright (c) 1993 - 2000 Compugen Ltd.
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pir2:*
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pir4:*
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   9, 2001, 15:36:29; Search time 54.37 Seconds (without alignments) 298.422 Million cell updates/sec
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                                           G81091
G81097
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T24928
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B65032
B72647
C83577
C83577
C83577
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beta-glucosidase (
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	ribosomal protein	50S ribosomal subu	ribosomal protein	hypothetical prote	thioredoxin C-2 -	hypothetical prote		hypothetical prote	pr	malX protein - Kle	hypothetical prote	neurotoxin Tx2 - s	ribosomal protein		hypothetical prote	myosin heavy chain	translation initia	translation initia	probable infB - My	translation initia	probable Na/H anti	

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elkl protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 16-Jul-1999
C;Accession: JC4965; I48339; I48340; S54908
R;Grevin, D.; Ung, S.; Denhez, F.; Dehem, M.; Quatannens, B.; Begue, A.; Stehelin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: xp11.2-xp11.2
C; Superfamily: elk-1 transforming protein; ets DNA-binding
C; Keywords: DNA binding; oncogene; transforming protein
F;7-86/Domain: ets DNA-binding domain homology <FTS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 318-328,'xx',331;336-364;380-388,'x',390-392,'x',394-400,'xx',403-405,'X'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: ERK phosphorylation potentiates Elk-1-mediated ternary complex formation and A; Reference number: S54721; MUID:95196758
A; Accession: S54721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Homo sapiens (man)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C:Accession: A41354; S54721
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EMBO J. 14, 951-962, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: elk, tissue-specific ets-related genes on chromosomes X and 14 near transloc A;Reference number: A41354; MUID:89203250 A;Accession: A41354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:119867; OMIM:311040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: ELK1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M25269; NID:g538208; PIDN:AAA52384.1; PII R;Gille, H.; Kortenjann, M.; Thomae, O.; Moomaw, C.; Slaughter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-428 < RAO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transforming
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8; Conser
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0; Mismatches
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er, C.; Cobb,
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Gene 174, 185-188, 19
A; Title: Structure ar
A; Reference number: 3
A; Accession: JC4965
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A;Map position: 16p12.3-16p12.3
C;Superfamily: mitochondrial processing peptidase alpha chain
C;Keywords: hydrolase; mitochondrial matrix; mitochondrion; oxidative phosphorylation;
E;1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>
E;15-453/Product: ubiquino1--cytochrome-c reductase core protein II #status predicted
                                        д
                                                                     Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubiquinol--cytochrome-c reductase (EC 1.10.2.2) core protein II precursor -C;Species: Homo sapiens (man) C;Date: 21-May-1990 #sequence_revision 14-Jul-1994 #text_change 16-Jul-1999 C;Accession: A32629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 70/3; 219/3; 363/3; 397/3
C;Superfamily: elk-1 transforming protein; ets DNA-binding
F;7-86/Domain: ets DNA-binding domain homology <ETS>
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A;Title: Net, a new ets transcription factor that is A;Reference number: A53837; MUID:95047310
A;Accession: I48339
                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:J04973; A; Note: the authors translated
                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-453 <HOS>
                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 264, 13483-13488, 1989
A;Title: Complementary DNA encoding core protein II of human mitochondrial cytochrome
A;Reference number: A32629; MUID:89340421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 5-132,'T',134-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X87257; NID:g836634; PIDN:CAA60715.1; PID:g836635
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A; Residues: 1-429 <GRE>
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                                                                                                                                                                                                                                                                                                                                                                                                                       Reference number: A32629; Accession: A32629
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Best Local S
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Residues: 1-429 <RES>
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                                        266 LVHAAFVA 273
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                                                                         LVHAAFVA 20
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8; Conser
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8; Conser
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ilarity 100.0%;
Conservative
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and (
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                                                                                                                           3.8%;
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Pred. No.
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hypothetical protein PA2722 [imported] c;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision C;Accession: D83305
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D83305
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C; Date: 25-Nov-1997 #sequence
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A; Residues: 1-850 <HIG>
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beta-2-microglobulin - guinea pig
N;Alternate names: class I histocompatibility antigen
C;Species: Cavia porcellus (guinea pig)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #te
C;Accession: A02181
R;Wolfe, P. B.; Cebra, J.J.
Mol. Immunol. 17, 1493-1505, 1980
                                                                                                          C:Superfamily: immunoglobulin C region; immunoglobulin C region; immunoglobulin homology <IMM>F;18-82/Domain; immunoglobulin homology <IMM>F;25-80/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                         A;Title: The primary structure of guinea pig beta2-microglobulin A;Reference number: A02181; MUID:82057805 A;Accession: A02181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Comment: This protein is a member of the epidermal growth ating the differentiation of MDA-MB-453 cells. C:Superfamily: unassigned EGF-related proteins; EGF homology C:Keywords: glycoprotein
                                                                                                                                                                                                                                 A; Residues: 1-99 <WOL> C; Complex: heterodimer with MHC class I histocompatibility antigen alpha chain
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F;345-381/Domain: EGF-like #status predicted F;346-381/Domains site: carbohydrate (Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biochem. 122, 675-680, 1997
A; Title: A novel brain-derived member of A; Reference number: JC5700; MUID:98006324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: DDBJ:AB005060; NID:g2626738; PIDN:BAA23417.1; PID:g2626739
A;Experimental source: SK-NSH cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, 675-680, 1997
Conservative 100.0%;
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                    3.3%; Score 7;
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Pseudomonas aeruginosa

15-Sep-2000

#text_change

31-Dec-2000 (strain PAO1)

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Copyright (c) 1993 - 2000 Comp
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                 ELKL_HUMAN
ELKL_MOUSE
UCR2_HUMAN
NRG2_HUMAN
VE7_HPV4
B2MG_CAVPO
RL22_LEPIN
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Q9zeal rickettsia	P39333 escherichia	P55151 macaca mula	P01236 homo sapien	088396 mus musculu	070627 mus musculu	060258 homo sapien	P49273 dermatophag	P43855 haemophilus	P13997 kluyveromyc	P41263 gallus gall	P46587 candida alb	P25654 saccharomyc	Q11088 caenorhabdi	070432 meriones un	P12140 oryza sativ	p06589 zea mays (m

ALIGNMENTS

RESULT ELKL_HUMAN OTSOAG, Q9UJM4; O95058; D1 NOV1990 (Rel. 16, Created) D1 O1-NOV-1990 (Rel. 40, Last sequence update) D1 O1-OCT-2000 (Rel. 40, Last sequence update) D1 O1-OCT-2000 (Rel. 40, Last sequence update) D2 O1-OCT-2000 (Rel. 40, Last sequence update) D3 O1-OCT-2000 (Rel. 40, Last sequence update) D5 O1-OCT-2000 (Rel. 40, Last sequence update) D6 E25-DOMAIN PROTEIN ELK-1. G8 ELK1. C9 Homo sapiens (Human). C0 Eukaryota; Metazoa; Chordata: Craniata; Vertebrated sequence update) G9 ELK1. C1 Homo sapiens (Human). C1 Kannalia; Eutheria; Primates; Catarrhini; Hominia C2 MCDE_TaxID=9606; RN [1] RN SEQUENCE FROM N.A. RR Red V.N., Huebbner K., Isobe M., Ar-Rushdi A., Cro RA Reddy E.S.P.; RN REDLINE=99013876; PubMed=2539641; RN RA RAD V.N., Huebbner K., Isobe M., Ar-Rushdi A., Cro RR Reddy E.S.P.; RN [2] RN [3] RN [4] RN [4] RN [5] RN [6] RN [7] RN [7] RN [8] SDUENCE FROM N.A. RA Aryee D.N.T., KOVAIT H.; RN [8] SDUENCE FROM N.A. (ISOFORM 2). RA Aryee D.N.T., KOVAIT H.; RN [8] SDUENCE FROM N.A. (ISOFORM 2). RA Aryee D.N.T., KOVAIT H.; RN [8] DMAINS. RN [8] RN [8] DMAINS. RN [8] RN [8] RN [8] RN [8] DMAINS. RN [8] PDMAINS. RN [8] MEDLINE=92334979; PubMed=1630903; Janknecht R., Nordheim A.; Janknecht R., Nordheim A.; "Elk-1 protein domains required for direct and SRF-assisted DNA-binding."; Nucleic Acids Res. 20:3317-3324(1992). -i- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FIGURE AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE MEDITINE-99013876; PubMed-9795224; Harindranath N., Mills F.C., Mitchell M.P., Meindl "The human elk 1 gene family: the functional gene pseudogenes embedded in the IgH locus."; Aryee D.N.T., Kovar H.; "Novel family members HuER71, ELFR, and ELKv among ETS-related Coexpressed with EWS-FLI1 in Ewing tumor cell lines "; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ELEMENT. SUBCELLULAR LOCATION: NUCLEAR. ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE), AND 2/ELKV; ARE the EMBL/GenBank/DDBJ databases Ar-Rushdi A., Croce C.M., genes on chromosomes X and and Α., , Max E.E.; two process processed 14

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RESULT 2
ELK1_MOUSE
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01-NOV-1995 (Rel. 3:
01-OCT-1996 (Rel. 3:
15-JUL-1999 (Rel. 3:
ETS-DOMAIN PROTEIN I
SEQUENCE OF 5-224 FROM N.A.
TISSUE-Embryo;
MEDLINE-95047310; PubMed=7958835;
Glovane A., Pintras A., Maira S.-M.,
"Net, a new ets transcription factor
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Pfam; PF00178; ETS; 1.
PRINTS; PR00454; ETSDOMAIN.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS00046; ETS_DOMAIN_3; 1.
PROSITE; PS00061; ETS_DOMAIN_3; 1.
PROSITE; PS00061; ETS_DOMAIN_3; 1.
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Interpro;
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                                                                                                                                   MEDLINE-97017146; PubMed-8863747; Grevin D., Ung S., Denhez F., Deh Stehelin D., Martin P.; "Structure and organization of th
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation; Alternative splicing.
DNA_BIND
5 86 ETS-DOMAIN.
VARSPLIC 91 95 VAGCS
VARSPLIC 96 428 MISSING (IN ISOFORM 2).
CONFLICT 183 183 S -> N (IN REF. 1).
SEQUENCE 428 AA; 44888 MW; 68F71F8ADB9D38CA CRC64;
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EMBL; AF080616; AAC62466.1; --
EMBL; AL009172; CAA15659.1; --
EMBL; AF000672; AAD00862.1; --
                                                                                                    Gene 174:185-188(1996).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL; TISSUE-Embryo;
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HSSP; P14921; 2STW.
TRANSFAC; T00250; -.
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TISSUE SPECIFICITY: LUNG AND TESTIS.
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(Rel. 34,
(Rel. 38,
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Last annotation updat
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    Sobieszczuk P., Wasylyk B.; that is activated by Ras.";
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X MEDLINE-89340421; PubMed-2547763;

XA MEDLINE-89340421; PubMed-2547763;

XA MEDLINE-89340421; PubMed-2547763;

XA HOSOKAMA Y., SUZUKİ H., TOĞA H., NİSHİKİMİ M., OZAWA T.;

XA HOSOKAMA Y., SUZUKİ H., TÖĞA H., NİSHİKİMİ M., OZAWA T.;

XI CYTOCHTOME DOL COMPLEX. SUBSTANTIAL ĞİVERSİTY İN DEĞÜLCEĞ PRIMATY

X STRUCTURE FROM İTS YEAST COMPONENT OF THE UBIQUINOL-CYTOCHROME C

XI DIOL CHAM. 264.13483-13486 (1989).

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Matches 8
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P22695;
01-AUG-1991 (Rel. 19, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
UB1QUINDL-CYTOCHROME C REDUCTASE COMPLEX CORE
(EC_1_10.2.2) (COMPLEX III SUBUNIT II).
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-!- FUNCTION: STIMULATES TRANSCRIPTION. BINDS TO PURINE-RICH DNA SEQUENCES. CAN FORM A TERNARY COMPLEX WITH THE SERUM RESPONSE FACTOR AND THE ETS AND SRF MOTIFS OF THE FOS SERUM RESPONSE ELEMENT.

-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN, AND LESSER EXTENT IN THE HEART, LIVER AND MUSCLE.

-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO00418; -.

Pfam; PF00178; Ets; 1.

PRINTS; PR00454; ETSDOMAIN.

PROSITE; PS00345; ETS_DOMAIN_1;

PROSITE; PS00346; ETS_DOMAIN_2;

PROSITE; PS00346; ETS_DOMAIN_3;
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EMBL; Z36939; CAA85391.1;
HSSP; P14921; 2STW.
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Q9eqf1 cavia porce
Q9i0C0 pseudomonas
Q9hvx4 pseudomonas
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Q9ev14 actinobacil
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O9rdf5 streptomyce
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Matches 8
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-!- SIMILARITY: TO
FAMILY.
                                                  Oxidoreductase.
SEQUENCE 276 AA;
                                                                                                   InterPro; IPR002198; InterPro; IPR002347;
 h 3.8%; Score 8; DB Similarity 100.0%; Pred. No. 2. 8; Conservative 0; Mismatches
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151 151 151 151 151 151 151 151 151 151
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Q9EUY4 Q9EUY3 Q9EUY1 Q9EUY0 Q9EUY0 Q9EUX9 Q9EUX7 Q9EUX7 Q9EUX3 Q9EUX3 Q9EUX3 Q9EUX3 Q9EUX3 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1 Q9EUX1
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PODO 7: Young G., Yoshikuni M., Nagahama Y.;

Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Nagahama Y.;

PCloning and expression of two carbonyl reductase-like 20beta-

Nydroxysteroid dehydrogenase cDNAs in ovarian follicles of rainbow trout (Oncorhynchus mykiss).";

Blochem. Biophys. Res. Commun. 255:123-128(1999).

-i- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9YGD6 PRELIMINARY; PRT; 276 AA.
Q9YGD6;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TrEMBLrel. 16, Last annotation update)
Q1-MAY-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE B.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID-8022;
                                                                                                                                                                                                                                                               EMBL; AF100930; AAD20217.1; HSSP; P50163; 2AE1.
                                                                     PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                              Pfam; PF00106; adh_short; 1.
30111 MW;
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135604A38D2940CD CRC64;
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DB 13; b. 2.8;

Length 276 Indels

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Gaps

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AFKNDATE

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Q9PT38;
Q1-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                    Q9PT37;
01-MAY-2000
01-MAY-2000
                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99185307; PubMed-10082666;
Guan G.J., Tanaka M., Todo T., Young G., Yoshikuni M., Y
"Cloning and expression of two carbonyl reductase-like ?
"Cloning and expression of two carbonyl reductase-like ?
                                                                                                                                                            Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. NCBI_TaxID-8022;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE
                                                                                                                                                                                                                                       01-WAY-2000 (TremBLrel. 13, Created)
01-WAY-2000 (TremBLrel. 13, Last sequence update)
01-WAY-2000 (TremBLrel. 16, Last annotation update)
01-WAR-2001 (TremBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                 Q9PT37
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BioChem. Biophys. Res. Commun. 255:123-128(1999).
-i- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002347; -. Pfam; PF00106; adh_short; 1. PRINTS; PR00081; GDHRDH. PRINTS; PR00080; SDRFAMILY.
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HSSP; P50163; 2AE1
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                              hydroxysteroid dehydrogenase cDNAs in ovarian fo
trout (Oncorhynchus mykiss).";
Biochem. Blopbys. Res. Commun. 255:123-128(1999)
-1- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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   AF100932;
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   AAD20991.1;
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InterPro: IPR002347; -.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00081; GDHRDH.
PRINTS; PR00080; SDRFAMILY.
Oxidoreductase.
SEQUENCE 276 AA; 30127 MW;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CARBONYL REDUCTASE/20BETA-HYDROXYSTEROID DEHYDROGENASE A.
                                             O9RDF5 PRELIMINARY; PRT; 499 AA.

O9RDF5; O1-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE TRANSPORT PROTEIN.

SCC77.03C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002198; -.
InterPro; IPR002347; -.
Pfam; PF00106; adh_short;
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Streptomyces coelicolor.
Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase. SEQUENCE 276 AA;
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PRINTS; PR00080; SDRFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ut (Oncorhynchus mykiss).";
chem. Biophys. Res. Commun. 255:123-128(1999)
SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASE
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                   Score
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213
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| SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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herapy; antisense therapy; fracture; bone mineralization.
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Matches 108
                         Brunkow ME,
Van Ness J,
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Winkler D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                          Galas DJ,
Winkler DG;
                                                                                                                                                                                                                                           transforming growth factor-beta; TGF-beta; binding protein;
herapy; antisense therapy; fracture; bone mineralization.
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                 98US-0110283
                                                                                                                             99WO-US27990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.7%; Score 108; DB 21; I 100.0%; Pred. No. 5.5e-105; O. Mismatches 0;
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                                        Kovacevich B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kovacevich
                                                                                                                                                                                                                                                                                      (BEER)
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                                          Mulligan
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                                          JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JT,
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WPI; 2000-412321/35

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Title:
Perfect score:
Sequence:
Total number of hits satisfying chosen parameters:
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                                                                                                                                Scoring table:
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                                                                                                                                                                                     US-09-668-021-14
213
                                                                                                                                                                                                                                                                            November 9, 2001, 15:35:25;
                                                                         212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                   Search time 47.66 Seconds (without alignments) 100.571 Million cell updates/sec
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26		24		22	21	20	19	18	17	16	15	14	13	12	11	10	9	· œ	7	6	· UT	4	ω	2		Result No.
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US-08-821-637-3	US-08-462-778-2	US-08-476-515A-13	US-08-652-877-13	US-09-342-084-10	US-08-737-248-7	US-09-096-071-2	US-08-892-692-2	-666	US-08-985-526-25	US-08-600-993A-30	US-08-245-511-30	US-08-836-791-5	US-09-188-930-289	US-09-188-930-162	US-08-220-272A-6	US-08-764-100-24	US-09-475-316A-13	US-08-370-476-61	US-08-481-985B-61	US-08-484-905-61	US-09-398-496-32	US-08-753-007A-32	US-09-188-930-286	US-09-188-930-159	US-08-468-847B-20	US-08-468-847B-2	ID
ω,	2, A	13,	13,	10,	7, Appl	2	2,		25,	30,	30	5, A	289,	162	6,	24,	13,	61,	61,	61,	32,	32, 7	286,	159,	Sequence 20, Appl	Sequence 2, Appli	Description

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Sequence 4, Appli Sequence 5, Appli	- 6	Sequence 6, Appli Sequence 6, Appli	Sequence 11, Appl Sequence 11, Appl	Sequence 11, Appl	2, ;	16,	•	11,	Sequence 1, Appli	•	Sequence 13, Appl	Sequence 278, App	Sequence 144, App	`	Sequence 33, Appl	•	Sequence 22, Appl	`

ALIGNMENTS

MOLECULE TYPE: PROTEIN
TODOLOGY: LINEAR STRANDEUNESS:
TYPE: AMINO ACID
LENGTH: 206 AMINO ACIDS
AND CHARLES AND ACT ACT ACT ACT ACT ACT ACT ACT ACT ACT
744
TELEPHONE: 201-994-1700
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REFERENCE/DOCKET NUMBER: 325800-442
NAME: MULLINS, J.G.
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FILING DATE:
APPLICATION NUMBER.
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FICATION: 435
FTI.ING DATE: 6 June 1995
ADDITION NUMBER: US /08 /468 8478
CHERRIA ADDITON DATA:
TORRED CROW
TRM PS/2
PE
COMPUTER READABLE FORM:
ZIP: 07068
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ROSELAND
BECKER FARM ROAD
ADDRESSEE: CECCHI, STEWART & OLSTEIN
CE ADDRESS:
Human CCN-Like Growth Fact
APPLICANT: Hastings, Gregg A. and Adams, Mark D.
GENERAL INFORMATION:
Sequence 2, Application US/08468847B
S-08-468-847B-2
ESULT 1

Length 206;

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Query Match
Best Local Similarity
Tatches 9; Conserv
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Thehes 9; Conserv
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US-08-468-847B-20
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                                                                                                                US-09-188-930-159
                                                                     Sequence 159, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
S-08-468-847B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08468847B Patent No. 5780263 GENERAL INFORMATION:
                         APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                      28 AFKNDATEI 36
                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 201 J. TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2
OPERATING SYSTEM: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6 BECKI
CITY: ROSELAND
STATE: NEW JER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILIAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
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23 AFKNDATEI 31
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ZIP: 07068
                                                                                                                                                                           23 AFKNDATEI 31
                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 206 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 6 June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
Murison, James Greg
            Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hastings,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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Human CCN-Like Growth Factor
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100.0%;
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100.0%;
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Pred. No.
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NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 159
LENGTH: 206
TYPE: PRT
ORGANIZM: mouse
US-09-188-930-159
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Best Local Similarity
Thehas 9; Conserve
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Best Local Similarity
Conserv
                                                                                                                                                                                                                     US-08-753-007A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mouse US-09-188-930-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-188-930-286
                                                                                                                                                                                  Sequence 32, Application US/08753007A Patent No. 6074841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 286
LENGTH: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 615050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compositions Isolated from Skin Cells TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                      APPLICANT: Gearing, David P.
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
                                                   CORRESPONDENCE ADDRESS:
                                                                     NUMBER OF SEQUENCES:
             STREET:
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CITY:
                                                                                                                                                                                                                                                                                              23 AFKNDATEI 31
                                  ADDRESSEE: Fish & Richardson P.C
Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09188930A
             225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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100.0%; Pred. No. 0.27;
ive 0; Mismatches
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b; Pred. No. 0.2
0; Mismatches
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COUNTRY: US ZIP: 02110-2804

STATE: MA

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Title:
Perfect score:
Sequence:
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Maximum DB
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match I	Length	В	ID	Description
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2	7	4.0	130	N	D83305	
ω	7	4.0	139	N	A82330	4
4	7	4.0	148	Ν	C83091	\circ
5	7	4.0	183	2	B37410	H
Φ	7	4.0	230	N	137095	gene 2.19 protein
7	7	4.0	321	2	в82892	erved
œ	7	4.0	325	N	T35023	CD.
9	7	4.0	328	N	S72647	hypothetical prote
10	7	4.0	341	N	S71223	xyloglucan endo-1,
11	7	4.0	343	N	B86446	probable endoxylog
12	7	4.0	398	_	S24802	polyferredoxin 6x2
13	7	4.0	426	N	T15285	hypothetical prote
14	7	4.0	521	N	S54266	
15	7	4.0	562	2	T05758	
16	7	4.0	573	N	в70942	
17	7	4.0	632	4سز	VGVNSY	Ω
18	7	4.0	864	2	JS0076	regulatory protein
19	7	4.0	1168	Н	MWAXIC	myosin heavy chain
20	7		1308	N	T15280	tical
21	7		1646	2	T40198	hypothetical SPBC3
22	7		3006	2	T28625	variant-specific s
23	7		6420	N	T30283	polyketide synthas
24	6	3.4	49	N	S29215	
25	6	3.4	65	N	B25025	malX protein - Kle
26	6	3.4		N	S41672	tightly associated
27	6	3.4	89	N	D75271	hypothetical prote
28	6	3.4	99	N	T17268	
29	6	3.4	105	2	H72708	Ö

50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30
6	σ	σ	0	ō	σ	O	σ	o	0	6	o	6	0	o	ō	6	6	ον	6	6
3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4	3.4		3.4	3.4	3.4	3.4
145	142	141	137	136	134	130	129	125	124	124	124	124	124	119	118	113	111	110	110	106
2	N	N	N	ν	N	Ν	N	N	4	4	N	Ν	щ	N	ν	2	N	Ν	ب	N
G69011	н72600	B81268	PC4297	T45360	D75534	E82647	T46388	T10936	JH0809	JH0807	臣85998	JH0443	R3EC12	JQ2032	T15239	S66512	C41839	н85996	R5EC22	A82560
hypothetical prote	hypothetical prote	508 ribosomal prot	cadherin FIB1 - hu	hypothetical prote	ribosomal protein	hypothetical prote	hypothetical prote	cellulase (EC 3.2.	ribosomal protein	ribosomal protein	30S ribosomal subu	ribosomal protein	ribosomal protein	lambda 208 protein	hypothetical prote	ribosomal protein	ribosomal protein	50s ribosomal subu	ribosomal protein	50S ribosomal prot

ALIGNMENTS

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C;Accession: D83305

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist A;Reference number: A82950; MUID:20437337

A;Accession: D83305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S14292
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <KUL>
C;Superfamily: GAL4 zinc binuclear cluster homology
E;7-54/Domain: GAL4 zinc binuclear cluster homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription activator - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Jul-1998
C;Accession: S14292
                A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-130 <STO>
A;Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AAG06110.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kulmburg, P.; Prange, T.; Mathieu, M.; Sequeval, D.; Scazzocchio, C.; Felenbok, B. FEBS Lett. 280, 11-16, 1991
A;Title: Correct intron splicing generates a new type of a putative zinc-binding doma A;Reference number: S14292; MUID:91184391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.0%; Score 7; DB: Best Local Similarity 100.0%; Pred. No. 11 Matches 7; Conservative 0; Mismatches
Genetics:
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A; Gene:
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A;Map position: 1
C;Superfamily: hy
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                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-148 <STO>
                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337 A;Accession: C83091
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;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.;
dman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.;
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein PA4441 [imported] - Pseudomonas aeruginosa (strain PAO1) C; Species: Pseudomonas aeruginosa C; Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A;Cross-references: GB:AE004126; GB:AE003852; NID:g9654802; PIDN:AAF93546.1;
A;Experimental source: serogroup O1; Strain N16961; biotype EI Tor
C;Genetics:
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A;Title: DNA Sequence of both chromosomes of
;Reference number: A82035; MUID:20406833
A;Accession: A82330
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein VC0373 [imported] - Vibrio cholerae (strain N16961 serogroup) C;Species: Vibrio cholerae (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: A82330
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26 ARLLPNA
                                     81 ARLLPNA 87
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H.; Dragoi, I.; Sellers,
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K.; Lim,
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A; Residues:
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conserved hypothetical UU417 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: B82992 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: 2.19
C;Superfamily:
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R;Bione, S.; Tamanini, F.; Maestrini, E.; Tribioli, C.; Poustka, Proc. Natl. Acad. Sci. U.S.A. 90, 10977-10981, 1993
A;Title: Transcriptional organization of a 450 kb region of the ha;Reference number: I37095; MUID:94068527
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137095
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C;Superfamily: class II histocompatibility antigen;
F;105-170/Domain: immunoglobulin homology <IMM>
                 A; Reference number: A82870
A; Accession: B82892
                                                          submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-230 <RES>
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C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
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A;Title: Structure of class II genes in wild mouse Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus saxicola
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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A; Residues: 1-183 < CAM>
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A; Status: preliminary
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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RL22_SPICI
RL22_THETH
TIAF_HUMAN
TIAF_MOUSE
REV_HV1LW
Y13K_NPVOP
      MPL_MPLV
HS72_CANAL
RETB_CHICK
TRPF_KLULA
DEOC_BACSU
FGFH_HUMAN
FGFH_MOUSE
PRL_HUMAN
                                                                                RS12_ECOLI
RL22_PHYS1
RK22_MAIZE
RK22_ORYSA
R19E_PYRHO
B3AR_MERUN
YCY0_YEAST
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MYSC_ACACA
TX25_PHONI
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219_HUMAN
VGLG_SYNV
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STANDARD;

PRT;

110

ΑA

рЬ QУ Query Match Best Local S Matches 7 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). STRAIN=SEROVAR LAI;
MEDLINE=20088835; PubMed=10620683;
MEDLINE=20088835; PubMed=10620683;
Zuerner R. L., Hartskeerl R. A., van de Kemp H., Bal A.E.;
"Characterization of the Leptospira interrogans S10-spc-Pfam; PF00237; Ribosomal L22; 1.
PROSITE; PS00464; RIBOSOMAL L22; 1.
Ribosomal protein; rRNA-binding.
SEQUENCE 110 AA; 12566 MW; B918; EMBL; AF115283; AAD40588.1; Leptospira interrogans 126 RKVRLVA 132 15 (BY SIMILARITY).
SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS. RKVRLVA 21 Similarity 7; Conser IPR001063; Spirochaetales; Conservative PROTEIN 39, 4.0%; Last sequence update)
Last annotation update) Leptospiraceae; Leptospira 0; Score 7; Pred. No. B9181B85E9756CAA CRC64; Mismatches . DB .2; 0; Length 110 S10-spc-alpha Indels 0, Gaps 0;

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RESULT 3
VGLG_SYNV
ID VGLG_
AC P2727
AC P2727
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219_HUMAN
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SIGNAL
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01-OCT-1996
01-OCT-2000
2-19 PROTEIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Fetal brain;
MEDLINE=94068527; PubMed=8248200;
Bione S., Tamanini F., Maestrini E., Tribioli C., Poustka A.,
Torri G., Rivella S., Toniolo D.;
"Transcriptional organization of a 450-kb region of the human
chromosome in Xq28.";
" G. N. an.10077-10081(1993).
VGLG_SYNV STP
P27277;
01-AUG-1992 (Rel.
                                                                                                                                                                                                                                                                                                                  modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                             EMBL; X55448; CAA39090.1; EMBL; X87193; CAA60645.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D'Urso M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zollo M., Mazzarella R., D'Urso M., Chen E.Y.;
                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G6PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zuo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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loci.";
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                                                                                                                                                                                                                230
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                                                                                                                                                                                                                                                                                                                                                                                                                                     HEART
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(Rel.
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                                                                                                                                                  Conservative
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PECIFICITY: IN SIMILAR AMOUNTS
PLACENTA, BRAIN, FETAL BRAIN,
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34, Last sequence up
40, Last annotation
  Created)
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Pred. No.
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2-19 PROTEIN.
FE3934D91F98CAAD
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                           PRT;
                                                                                                                                                  Mismatches
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BRAIN, LIVER, KID
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RESULT 4
ALCR_EMENI
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Best Local
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P21228;
01-MAY-1991 (Rel. 1
01-NOV-1995 (Rel. 3
01-OCT-2000 (Rel. 4
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Virology 185:32-38(1991).

-i- function: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.

-i- function: THIS PROTEIN FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE HOST CELLS AND FOR INDUCING THE UPPAKE OF THE VIRUS BY THE CELL.

THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND THE PORTION OF THE GLYCOPROTEIN EXPOSED ON THE CYTOPLASMIC FACE OF THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viruses; ssRNA negative-strand viruses;
Rhabdoviridae; Nucleorhabdovirus.
NCBI_TaxID=11307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L32603; AAA50384.1; EMBL; M73626; AAA47898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC PV-263;
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                                                            Emericella nidulans (Aspergillus nidulans)
Eukaryota; Fungi; Ascomycota; Pezizomycoti
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure of the glycoprotein gene of sonchus yellow net virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jackson A.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldberg K.B., Modrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92024089;
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SEQUENCE FROM N.A MEDLINE=89211976;
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17 POTENTIAL.
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40, Last annotation updat
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 PubMed=3072264;
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Perfect score:
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Q9RKH
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Q38908
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Q9RJY3
Q00388
Q19348
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O9hvx4 pseudomonas
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O9rky8 streptomyce
O9ibj1 turkey herp
O9xx119 arabidopsis
O9pq72 ureaplasma
O9xam5 streptomyce
O38908 arabidopsis
O9fvr2 arabidopsis
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O19348 caenorhabdi
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O9gtj4 ancylostoma
Q9i0c0 pseudomonas
Q9kuy5 vibrio chol
O9hvx4 pseudomonas
Q21999 bacteriopha
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ALIGNMENTS

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Q9HC30;
Q9HC30;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
02AMP SPECIFIC PHOSPHODIESTERASE VARIANT PDE4A-10 (FRAGMENT).
                                                                                                                                                                                         Sullivan M., Rena G., Begg F., Olsen A.S., Houslay M.D.;
"PDEAA-10, a novel human 5' splice variant of the cAMP specific phosphodiesterase PDEA gene.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF178570; AAG13806.1; -.
NON TER
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487 MW; A9A65DE55DD1283D CRC64;
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Sullivan M., Rena
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              PRT;
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Q9GTJ4;
Q1-MAR-2001
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLrel. 16, Last annotation update)
GENOMIC DNA, CHROMOSOME 5, TAC CLONE:K1L20.
Arabidopsis thaliana (Mouse-ear cress).
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STRAIN-COLUMBIA;
MEDLINE-20181125; PubMed-10718197;
CT+C S., Nakamura Y., Kaneko T., K
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YOLKOff N.A., Rocher J., Cerutti P., Ohresser M.C.,

Yolkoff N.A., Rocher J., Cerutti P., Ohresser M.C.,

Yolkoff N.A., Rocher J., Cerutti P., Ohresser M.C.,

Yolkoff N.A., Rocher J., Cerutti P., Ohresser M.C.,

Persistent expression of a newly characterized Hyposoter

PolyDNAvirus gene in long-term infected lepidopteran cell

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF241775; AAR91314.1; -

SEQUENCE 106 AA; 11821 MW; D810A541DA90A29C CRC64;
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                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
2INC METALLOPEPTIDASE 3 MEP3 (FRAGMENT).
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Viruses; dsDNA viruses, nc
NCBI_TaxID=96779;
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen M.Y.;
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SEQUENCE
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HYPOTHETICAL VC0373.
                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 130 AA; 1
                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Pseudomonas opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004700; AAG06110.1; -.
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Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
NCBI_TaxID=29170;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
6: /SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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14: /SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
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176
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SUMMARIES
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133.791 Million cell updates/sec
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16	32	ω	76	76	76	76	76	76	115	176	Score
9.1	18.2	18.8	43.2	43.2	43.2	43.2	43.2	43.2	65.3	100.0	% Query Match I
50	211	213	367	213	213	213	213	213	213	176	% Query Match Length DB
20	21	21	21	22	21	21	21	21	21	21	: BB
AAY12009	AAY96432	AAY96433	AAB26105	AAY97589	AAY96436	AAY96430	AAY96429	AAB26106	AAY96431	AAY96434	ID
Human 5' EST secre	Murine TGF-beta bi	Rat TGF-beta bindi	Human DAN/Cerberus	Human secreted pro	Human TGF-beta bin	Human TGF-beta bin	Human TGF-beta bin	Human DAN/Cerberus	Vervet TGF-beta bi	Bovine TGF-beta bi	Description

	49					44		42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	
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110	109	99	95	89	89	87	85	83	79	74	73	70	69	68	64	59	55	54	53	50	46	45	44	44	29	26	20	13	12	12	343	311	282	273	265	264	230	219	
21	21	21	21	21	21	20	20	21	20	21	21	21	21	17	21	22	21	21	21	20	21	21	20	19	19	20	13	7	10	6	21	22	21	21	21	21	21	21	
602	326	074		10	AAB51453	1 1	AAY74211	AAY52138	AAY73911	AAG19051	AAB52618	AAG13972	AAG13973	AAR95687		AAB87776	AAB40943	AAG41013	AAG01311	AAY30853	AAB54384	AAB38165	AAW74042	AAW69242	AAY21475	AAY19646	AAR27052	AAP60742		AAP50474	AAG15727	6215	228	72	228	AAG15729	84	AAG42285	
E. coli proliferat	protei	D.	dopsis tha	secreted	secrete	normal pa	prostate	Human TANGO 125a (ostate tu	Zea mays protein f	н		<u>_</u>	Human GAP-SH3 doma	secret	Human T2R46 amino	an ORFX ORF	Zea mays protein f	secreted	secreted	pancreati		D2H binding		euroend	64 fro	N-terminal prolact	=	ctin	S.	ra	aru	Arabidopsis thalia	is thali	is tha	lopsis tha	okine fa	Arabidopsis thalia	

ALIGNMENTS

RESULT 1
AAY96434
ID AAY964

AAY96434 standard; Protein;

176 AA

Bovine TGF-beta binding protein (BEER).

12-SEP-2000 (first entry)

AAY96434;

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WPI; 2000-412321/35.
               Brunkow ME,
Van Ness J,
                                                                                                                                       osteopathic; transforming growth factor-beta; TGF-beta; binding protein; BEER; gene therapy; antisense therapy; fracture; bone mineralization.
                                                        27-NOV-1998;
                                                                        24-NOV-1999;
                                                                                        08-JUN-2000.
                                                                                                         W0200032773-A1
                                                                                                                         Bos taurus.
                                       (DARW-) DARWIN DISCOVERY LTD.
               Galas DJ, |
Winkler DG;
                                                        98US-0110283
                                                                        99WO-US27990
                       Kovacevich B,
                        Mulligan JT,
                       Paeper BW;
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RESULT
AAY96431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 127; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia,
WPI; 2000-412321/35
                           Brunkow ME,
Van Ness J,
                                                                                                        27-NOV-1998;
                                                                                                                                      24-NOV-1999;
                                                                                                                                                                                                  WO200032773-A1
                                                                                                                                                                                                                              Cercopithecus pygerythrus
                                                                                                                                                                                                                                                                            osteopathic; transforming growth factor-beta; TGF-beta; binding protein;
                                                                                                                                                                                                                                                                                                        Vervet TGF-beta binding protein (BEER).
                                                                                                                                                                                                                                                                                                                                        12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                       AAY96431
                                                                                                                                                                                                                                                                                                                                                                                                     AAY96431 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis and fractures
                                                                       (DARW-) DARWIN DISCOVERY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AAPRARKVRLVASCKCKRLTREHNQSELKDFGPEAARPQTGRKLRPRARGTKASRA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPCRSAKPVTELVCSGQCGPARLLPNAIGRGKWWRPSGPDFRCIPDRYRAQRVQLLCPGG 120
                                                                                                                                                                                                                                                           gene therapy; antisense therapy; fracture; bone mineralization
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                           Galas DJ,
Winkler D
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                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                        98US-0110283
                                                                                                                                      99WO-US27990
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                             g;
                                            Kovacevich B,
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                                            Mulligan
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                                            JT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                            Paeper BW;
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                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 This shows a vervet transforming growth factor-beta (TGF-beta) binding protein designated vBEER. The cDNA and protein may be used for prevention, treatment and diagnosis of diseases associated with inappropriate BEER expression. For example, they may be used to treat disorders associated with decreased TGF-beta BP expression. The cDNA or vectors may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of BEER by expressing inactive proteins or to supplement the patients own production of BEER polypeptides. The nucleic acids may be used for recombinant production of BEER, gene therapy, antisense therapy, as probes for adiagnostic assays and for functional studies. BEER may be used to raise antibodies and for identification of BEER modulators. BEER antagonists may be used to increase bone mineral content for the treatment of disorders such as osteopenia, osteoporosis, fractures and other disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 122-123; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids (I) encoding a transforming growth factor beta binding protein, useful for identifying agents for treating osteopenia,
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                    associated with low mineral content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
AAB26106 standard; Protein;
                                                                                        105 PDRYRAQRVQLLCPGGAAPRARKVRLVASCKCKRLTRFHNQSELKDFGPEAARPQ 159
                                                                                                                                                                  AAA29057
                                                                                                                                                                                                                                                                                                                                             213 AA;
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                 65.3%;
    213
                                                                                                                                                                                                                                                 Score 115; DB 21;
; Pred. No. 3e-111;
0; Mismatches 0;
  AA
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                                                                                                                                                                                                                                                     Indels
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0;

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Human; DNA/Cerberus-related protein 6; hDCR6;
antagonist; BMP; cell growth; cell differentia
Novel isolated, human DNA/Cerberus related protein 6 which include natural homologue, and polypeptides comprising DCR6 domain and nuc
                              WPI; 2000-638179/61.
N-PSDB; AAA94051.
                                                                                                                               02-MAR-2000; 2000WO-US05537
                                                                                                                                                                                                                    gene therapy.
                                                                                                                                                                                                                                                              Human DAN/Cerberus-related protein 6 (hDCR6) (exons 1 and
                                                                                                                                                     21-SEP-2000
                                                                                                                                                                          WO200055193-A2
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                    15-JAN-2001 (first entry)
                                                                Economides
                                                                                    (REGE-) REGENERON PHARM INC
                                                                                                          12-MAR-1999;
                                                                                                          99US-0124118
                                                                                                                                                                                                                                rotein 6; hDCR6; morphogenic protein;
cell differentiation; bone formation;
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Result
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Perfect score:
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      22222221111111198765432
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DB seq length: 2000000000
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Match
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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25, Appl
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APPLICANT: WERKULOV, Gennady et al
APPLICANT: WERKULOV, ISOLATED HUMAN PROTEASE PR
TITLE OF INVENTION: NUCLEIC ACID MOLECULES EN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001177
CURRENT APPLICATION NUMBER: US/09/813,819
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 855
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US-09-813-819-2
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ENCODING

HUMAN PROTEASE PROTEINS,

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RESULT 2
US-08-078-311-25
                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Human
US-09-813-819-2
                                                                                                                                                                            Sequence 25, Application US/08078311 Patent No. 5925750
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Penciolel APPLICANT: Souyri, w APPLICANT: Tambourin APPLICANT: Variet, F APPLICANT: Vigon, Is APPLICANT: Wendling, TITLE OF INVENTION:
                                                                                                                              APPLICANT;
                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                          772 ARGTKAS 778
                                                                                                                                                                                                                                                                                             168 ARGTKAS 174
                         Varlet, Paule
Vigon, Isabelle
Wendling, Francoise
                                                                                                           Charon, Martine
Gisselbrecht, Silvie
Penciolelli, Jean-Francios
                                                                              Souyri, Michele
Tambourin, Pierre
                                                                                                                                                                                                                                                                                                                                        Conservative
 Polypeptide of a Growth Factor Receptor Family, Application in the Diagnosis and Treatment of
                                                                                                                                                                                                                                                                                                                                      100.0%; F
tive 0;
                                                                                                                                                                                                                                                                                                                                    4.0%; Score 7; DB 4
.00.0%; Pred. No. 69;
.ve 0; Mismatches
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Best Local Similarity Tarches 6; Conservat
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                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                             08-460-402-25
                                                                                                                                                                                                                                                                                                    tent No. 596300.
Theral INFORMATION:
                                                                                                              APPLICANT: Vigon, Isabelle
APPLICANT: Wendling, Francoise
APPLICANT: Wendling, Francoise
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 LRPRAR 169
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STATE: MN
COUNTRY: USA
                                                          STREET: 90 South CITY: Minneapolis
                                 COUNTRY:
                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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90 South 7th Street, 3100 No. 5989833west Center
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Vigon, Isabelle
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Penciolelli, Jean-Francios
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N: 435
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100.0%; Pred. No. 37;
tive 0; Mismatches
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o. 37;
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; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Extracellular domain of v-mpl
US-08-460-402-25
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Best Local Similarity
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TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charon, MA
APPLICANT: Gisselbree
APPLICANT: Penciolell
APPLICANT: Souyri, M.
APPLICANT: Tambourin,
APPLICANT: Variet, PR
APPLICANT: Variet, PR
APPLICANT: Wendling,
TITLE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITTILE OF INVENTION: ITT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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TELEPHONE: 612-332-5300
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APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 LRPRAR 169
                                                                                                      COUNTRY: U
ZIP: 55402
                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 01
FILING DATE: 18-JUN-1993
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                                                                                                                                                                                                     CITY: Minneapolis
                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LRPRAR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                                                                                      E: Merchant & Gould
3100 No. 5925750west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vigon, Isabelle
Wendling, Francoise
                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penciolelli, Jean-Francios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gisselbrecht,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Souyri, Michele
Tambourin, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Varlet, Paule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charon, Martine
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                      Polypeptide of a Growth Factor Receptor Family, Application in the Diagnosis and Treatment of Myeloproliferative Disease
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lo. 37;
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E: Floppy disk IBM PC compatible